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OM nucleic - nucleic search, using sw model

Run on: October 30, 2003, 04:33:40 ; Search time 114 Seconds  
(without alignments)  
8668.920 Million cell updates/sec

Title: US-09-667-170A-440

Perfect score: 2239

Sequence: 1 ggaggttgagtgagcagag.....ttattataaaaaaaaaaaaaa 2239

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	366.4	16.4	2072	2	US-09-073-362-2
2	366.4	16.4	2072	2	US-09-243-920-2
3	238.4	10.6	3984	4	US-09-016-434-1199
4	229	10.2	1564	4	US-09-489-847-11
5	211.4	9.4	1011	2	US-08-825-781-2
6	94.2	4.2	1578	4	US-09-107-532A-2089
7	89.2	4.0	1254	4	US-09-107-532A-347
8	67.4	3.0	7218	1	US-08-232-463-14
9	51.6	2.3	62804	3	US-09-800-960-3
10	50	2.2	152331	3	US-09-128-155-16
11	48.6	2.2	148567	4	US-09-801-876B-3
12	47.4	2.1	9862	4	US-09-691-861A-3
13	46.8	2.1	14485	4	US-09-876-216-3
14	44.8	2.0	6124	4	US-08-213-419B-3
15	44.2	2.0	64467	4	US-08-803-671B-3
16	43.6	1.9	5375	3	US-08-757-223-7
17	43.4	1.9	893	4	US-09-370-838-166
18	43.4	1.9	40000	4	US-09-780-049-18
19	43	1.9	83450	4	US-09-811-469-3
20	43	1.9	99500	4	US-09-798-096-10
21	43	1.9	162450	4	US-09-345-882-1
22	42.8	1.9	64467	4	US-09-803-671B-3
23	42.8	1.9	70000	4	US-09-851-896-3
24	42.8	1.9	72604	4	US-09-268-992-7
25	42.8	1.9	72604	4	US-09-657-474-7
26	42.8	1.9	148567	4	US-09-801-876B-3
27	42.6	1.9	3224	3	US-08-965-729A-2

Sequence 1, Appli  
Sequence 3, Appli  
Sequence 11, Appli  
Sequence 22, Appli  
Sequence 7, Appli  
Sequence 7, Appli  
Sequence 14, Appli  
Sequence 23, Appli  
Sequence 43, Appli  
Sequence 43, Appli  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 6, Appli  
Sequence 1, Appli  
Sequence 24, Appli

## ALIGNMENTS

RESULT 1  
US-09-073-362-2  
; Sequence 2, Application US/09073362  
; Patent No. 5942399  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA: US/09/073,362  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cerrone, Michael C  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0514 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2072 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: BSOGTUT02  
; CLONE: 2667831  
US-09-073-362-2

Query Match 16.4%; Score 366.4; DB 2; Length 2072;  
Best Local Similarity 54.6%; Pred. No. 5.6e+89;

Matches	730;	Conservative	0;	Mismatches	606;	Indels	0;	Gaps	0;
Qy	300	CGCCTTTTTCAGGAAGACGCGCTTTTTCAGGAAGAGAGAAAGTGCGAGCTGAAGAGAAAGT	359						
Db	192	CTCCCTTTTGGGTGATGGGCCAGCCCAAGCCGCGGACGAGCTGAAGCTGAAGAAGAGAT	251						
Qy	360	CACTTTACTGAGGGAGTCTCCATTATCATTTGGCACCATCATCTTGGAGCAGGAATCTTCAT	419						
Db	252	CTCATCTGCTTAACCGCGTGTCCCTGATTGTGGGAACATGATCGCTCAGGCATCTTTGT	311						
Qy	420	CTCTCTAAGGCGTGTCCAGAACAGCGGCAGGTGGCATGTCTCTGACCATCTGCAC	479						
Db	312	TTCCCCCAAGGTGTGCTCATACAGTGCCTCTTTTGGTCTCTCTCTGTFCATCTGGC	371						
Qy	480	GGTGTGGGGTCCGTCACTATTGGAGCTTCTTCTATTGCTCAAAATTGGGAAACAATAT	539						
Db	372	TGTCGGGGCCCTCTCTCCGTCCTTTGGGGCCCTTTGTTATGCGGAACTGGCACCAAT	431						
Qy	540	AAAGAAATCTGGAGGTCAATACATATATTTTGGAAAGTCTTTGGTCCATTAACAGCTTT	599						
Db	432	TAAAGAAATCTGGGGCAGCTATAGCTATATCCTGGAGGCTTTTGGAGGAAATTCCTTGT	491						
Qy	600	TGTACGAGTCTGGTGGAACTCCTCAATAACGCCCTGCACCTACTCTGTGATATCCCT	659						
Db	492	CATCAGACTCTGGACCTCCCTGCTCATCTTTGAGCCACACAGCAGGCCATCATTTGCCAT	551						
Qy	660	GGCATTTGGACGTACATTTCTGGAACCACTTTTATTCAATGTGAAATCCCTGAACTTGC	719						
Db	552	CACCTTTGCCAACTACATGTTACAGCCCTCTCTCCCGAGCTGCTTCGCCCTTATGCTGC	611						
Qy	720	GATCAAGCTCATTTACAGCTGTGGGATAACTGTGTAGTGAATGCTCTTAATAGCATGATGT	779						
Db	612	CAGCGGCTGTGCTGCTGCTGCATTTGTCTCTTAACTTCATTAACCTGTGCTGCTATGT	671						
Qy	780	CAGCTGGAGCGCCGGATCCAGATTTCTTAACTTTTGGCAAGCTCACAGCAATTTCTGAT	839						
Db	672	CAAAATGGGAACCTTGTTACAGATATTTTCCACTATGCTAAAGTATTTGGCACTGATCGC	731						
Qy	840	AAATATAGTCCCTGGAGTTATGCACTAAATTAAGGTCAACGAGAACCTTTAAAGACGC	899						
Db	732	GGTCATCGTTGCAGGCATTTGTAGACTTGGCCAGGAGCCCTCTACTCATTTTGAAATTC	791						
Qy	900	CTTTTCAGGAAGAGATTCAGATATTAACGGGTTGCCACTGGCTTTTATTATGGAATGTA	959						
Db	792	CTTTGAGGGTTTCATATTGCACTGGGTGACATTTGCCCTGGCACTGACTCAGCTCTGTT	851						
Qy	960	TGCATATGCTGGCTGGTTTTTACCTCAACTTTGTACTGAAGAAGTGAAGAACCCCTGAAA	1019						
Db	852	CTCCTACTAGGCTGGGACACCCCTCAACTATGTCACTGAAGAGATCAAGAAATCTCGAG	911						
Qy	1020	AACCATTTCCCTTTGCAATATGATATATCCATGGCCATTTGTCACCATTTGGCTATGTCTGAC	1079						
Db	912	GAACTGCCCTCTCCATGSCATCTCCATGCCATTGTCAACCATCATCTATATCTTTGAC	971						
Qy	1080	AAATGTGGCCTACTTTACGACCATTAATGCTGAAGAGCTGTGCTTTCAAATGCAAGTGGC	1139						
Db	972	CAATGTGGCCTATTATATGTGTCTAGACATGAGAGACATCTTGGCCAGTGTGCTGTTGC	1031						
Qy	1140	AGTCACCTTTTCTGAGCGGCTACTTGGGAAATTTCTATTAGCACTTCGATCTTTGTTGC	1199						
Db	1032	TGTGACTTTTTCAGATCAGATATTTTGGAAATTAATTAATCTGGATTAATTCACCTGTCAGTTGC	1091						
Qy	1200	CCTCTCTGCTTTGGCTCCATGAACGGTGTGTGTTGCTGTCTCCAGGTTATTTCTATGT	1259						
Db	1092	ATTATCTGTTTTTGGTGGCCTCAATGCCCTCCATTTGTGGCTGCTTCTAGGCTTTCTTTGT	1151						
Qy	1260	TGCGTCTCGAGAGGCTACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACAC	1319						
Db	1152	GGGCTCAAGAGAAAGCCATCTCCCTGATGCCATCTGCAATGATCCATGTTGAGCGGTTTCC	1211						
Qy	1320	TCCTCTACAGCTGTTATTGTTTGGACCCCTTTGACAAATGATTAATGCTCTTCTCTGAGA	1379						
Db	1212	ACCAAGTCCCTCTCTGCTCTTCAATGGTATCATGGCATTTGATCTACTTTGTCGTTGAAGA	1271						

QY	1380	CCTCGACAGTCTTTTGAAATTCCTCAGTTTTCGCGAGTGCGCTTTTATTTGGCGTGCAGT	1439
DB	1272	CATCTCCAGCTCATTTAACTACTACAGCTTCAGCTACTGGTCTCTTTGTGGGGCTTTCTAT	1331
QY	1440	TGCTGGGCTGATTTATCTTCGATACAAATGCCAGATATCATCGTCCTTTTCAAGGTGCC	1499
DB	1332	TGTGGGTCACTTTATCTCGGCTGGGAAGAGCTGATCGACTTCGTCCTCCCTCAGCTCAG	1391
QY	1500	ACTGTTTCATCCGAGTTTGTTTTCCTTTCACATGCCTCTTCATGTTTGCCCTTTCCCTCTA	1559
DB	1392	CGTTTTCTTCCCGATTGTCTTCTGCGCTCTGCACCATCTTCCTGGTGGCTGTTCACCTTTA	1451
QY	1560	TTCGGACCCATTAGTACACGGATGGCTTCCTGCATCACTCTGACTGGAGTCCCTGCGTA	1619
DB	1452	CAGTGATACATCAACTCCCTCATCGGCATTGCATTGCCCTCTCAGGCGCTGCCCTTTTA	1511
QY	1620	TTATCTCTTTTATATA	1635
DB	1512	CTTGCTCATCATCAGA	1527

RESULT 2  
US-09-243-920-2  
; Sequence 2, Application US/09243920  
; Patent No. 5981242  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/243,920  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/073,362  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cerrone, Michael C  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0514 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2072 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: ESOGTUT02  
; CLONE: 2657831  
US-09-243-920-2

Query Match	16.4%	Score 366.4;	DB 2;	Length 2072;
Best Local Similarity	54.6%;	Pred. No. 5.6e-89;		
Matches 730; Conservative	0;	Mismatches 606;	Indels 0;	Gaps 0;









/ FILING DATE: July 2, 1997  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Ariniello, Pamela Deneke  
/ REGISTRATION NUMBER: 40,489  
/ REFERENCE/DOCKET NUMBER: GTC-012  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (781)893-5007  
/ TELEFAX: (781)893-8277  
/ INFORMATION FOR SEQ ID NO: 2089:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 1578 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: double  
/ TOPOLOGY: circular  
/ MOLECULE TYPE: DNA (genomic)  
/ HYPOTHETICAL: NO  
/ ANTI-SENSE: NO  
/ ORIGINAL SOURCE:  
/ ORGANISM: Enterococcus faecium  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ LOCATION: (B) LOCATION 1...1578  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2089:  
US-09-107-532A-2089

Query Match 4.2%; Score 94.2; DB 4; Length 1578;  
Best Local Similarity 44.5%; Pred. No. 1.3e-15;  
Matches 528; Conservative 0; Mismatches 638; Indels 21; Gaps 3;

327 AGAAGAGAGAAAGTCAGCTGAAGAGGAAAGTCATTTACTGAGGGAGTCTCCATTAT 386  
Db 261 AGTAAATAGAAATGAATTAAGCGTACGATGGGATTTTTTACTGCTTTATCGACTGT 320  
387 CATTTGCACCATCATTTGGGACGAGATCTTCATCTCTCTAAGSGGTCTCCAGAAC 446  
Db 321 TATGGCACAAGTATCGGTGAGGGATTTTTTAAAGCGCAAGCGTAGCAGAAATTAC 380  
447 GGGCAGCGTGGGCATGCTCTGACCATCTGACCGGTGTGTGGGTCTCTGTCATATTGG 506  
Db 381 AGGATCGGCAGATTGTCATATGTTTCTTGTTCTCGGTGGTATGATTTCTGTCGTC 440  
507 AGCTTTGCTTATGCTGAATTTGGAAACAATAAAGAAATCTGGAGGTCATPACACATA 566  
Db 441 AGGACTAAACAGGAGCTGAATGCGAGCTGCTATTCAGAAACAGAGGAGGATGATTAATA 500  
567 TATTTTGGAGTCTTTGGTCCATTACAGCTTTTGTACAGTCTGAGTGGTGAATCTCAT 626  
Db 501 TATCGAACGGAATTACGGAATACAGAGCTTTTTTATTTGGGTGGGCGCAAGTCTGTAT 560  
627 AATACGCCCTGCAGCTACTGCTGTATATCCCTGGCATTTGGACGCTACATTTCTGAAAC 686  
Db 561 TTATTTTCCAGCAATAGTAGCAGCTTGTGATCATTTTTCGGTACAGTTCGTCAATCT 620  
687 ATTATTTATCAATGTAATGAAATCCCTGAACTTTGGATGCAAGCTCATPACAGTGTGGCAT 746  
Db 621 ATTGTGCTTTCCAGTCAAT-----GATTTTCCGTAGCTGTTACAGCTGC 668  
747 AACTGTAGTATGCTCTCTAAATAGATGATGATGATGATGATGATGATGATGATGATGAT 806  
Db 669 TGTATCGATCTCTGATCAATTTTATAGTCTTAAAGCTGAGGGGCTTTTCAGTCGAT 728  
807 CTTAACGCTTTTCAAGCTCACAGCAATTTCTGATAATTAATAGTCCCTGGAGTATGACGCT 866  
Db 729 TAGCGTTGCTGCAAGCTATTCTCTTTGTTGATGATGATGATGATGATGATGATGATGAT 788  
867 AATTAAGGTCAACCGCAGAACTTTAAAGACGCTTTTTCAGGAAGAGATCAAGTATTAC 926  
Db 789 AGAAGAGTAGACTTCCAACTGTTCCGATCCCAAGCAGGAGAAATCTTTCAATTTTCTC 848  
927 GCGGTTGGCACTGGCTTTTATATGGAATGATGATGATGATGATGATGATGATGATGATGAT 986  
Db 849 AGCCTTTGGAGCGGGCTTGTAGCAACGATGTTGCGCATACAGCGTTGGATACACGTAGG 908

987 CTTTGTACTGAAGAGTAGAAAAACCCGAAAAACCATTCCTCCCTTGCATATGTATATC 1046  
Db 909 AATATATTTGGGAGAAATTCAAAAAGCCGCGGAAAGATTTGCCAAAGCAATTTCTTTAGG 968  
1047 CATGGCCATTTGTACCATTTGGCTATGTCTGACAAATGTGCAAAATGTGGCTACTTTTACCAACATTAA 1106  
Db 969 AATCATCGGAATCATGATCGTTTATTTATTAGTAATGCGGTGTTCTTTAAGAACCGCATC 1028  
1107 TGCTGAGGAGCTGCTGCTTTTAAATGCGAGTGGCAGTACCTTTTCTGAGCGGCTACTGGG 1166  
Db 1029 TATCAGCGAGTTCGAGGAAACAGCAATGCGGCAAGTGCAGCTTGCAAAAATGATTTTGG 1088  
1167 AATTTCTCATTTAGCAGTTCCGATCTTTGTTGCC---CTCTCTGCTTTTGGCTCCATGAA 1223  
Db 1089 CGGCTTCGGTGAAGACTGGTCAAGTTGGTATCTTGATTTCTGTTTATGGAACCATCAA 1148  
1224 CGGTGGTGTGTTTGTCTCCAGTTATTTCTATGCTGCGTCTCGAGAGGTCACCTTCC 1283  
Db 1149 TGGCTATACCTTACTGGAATGCGTCTCCCTTATGTTATGGCAAAAGAAACACACCTGCC 1208  
1284 -----AGAAATCCTCTCCATGATTCATGTCGCGAGCACACTCTCTACAGCTGTTAT 1337  
Db 1209 TTTTAGCAAGCTCTTTGCTAAACCTTCATGATAAACTAAAGTTCTGTAGCGCGAGTAT 1268  
1338 TGTTTTGCACCCCTTTGACAAATGATATGCTCTCTCTGAGACCTCGACAGTCTTTTGA 1397  
Db 1269 CTTAGAGCTAGTCATCGCTATTTGGCATGATGATGATGATGATGATGATGATGATGATGAT 1328  
1398 TTTCTCAGTTTTCAGGTTGGCTTTTATTTGGGCTGGCAGTTGCTGGGCTGATTTATCT 1457  
Db 1329 TATGCTGATCTTTGTCAATTTGATTTTATACGATGCTTTTGTGGTGTCTCTCTCTCTCT 1388  
1458 TCGATACAAATGCCAGATATGCATGCTCTCTCTGAGACCTCGACAGTCTTTTGA 1504  
Db 1389 TCGTAAAAAGAAACCTGATTTGTTTCGACCATACAAAGTTCCAATGT 1435

RESULT 7  
US-09-107-532A-347  
; Sequence 347, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 347:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1254 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...1254  
SEQUENCE DESCRIPTION: SEQ ID NO: 347:  
US-09-107-532A-347

Query Match 4.0%; Score 89.2; DB 4; Length 1254;  
Best Local Similarity 44.2%; Pred. No. 2.7e-14;  
Matches 523; Conservative 0; Mismatches 638; Indels 21; Gaps 3;  
332 GAGAGAAAGTCAGCTGAAGGAAAGTCACCTTACTGAGGGAGTCTCCATTATCATTTG 391  
38 GAATGAAAGGCAACTAAACGAGAAATCAATCTGTTGGCGCATAGCTACCGTTATGG 97  
392 GCACCATCATTTGGAGCAGGAATCTTCTATCTCTCTTAAGGGGTGCTCCAGAACACGGGCA 451  
98 GAACCGTGATCGGTGACGGCTCTTCTCAAACTGCTGTTACTGCTAGTACTCAGT 157  
452 GCGTGGGCAATCTCTGACCACTCTGGACGGTGTGTGGGGTCTGTCACATATTTGGAGGTT 511  
158 CTACAAGTTTGACATTTGACATTTGCTTGGCTTTGGGTGTTTCTTAACGATCTGTGCTGGAT 217  
512 TGTCTTATGCTGAATTTGGAACTAATAAGAAATCTGGAGGTCAATTTACACATATATTT 571  
218 TGACAGTGGCTGAATTTAGCTACAGCAATCCCGGAACTGGTGGAGCTGTAAATATATTTG 277  
572 TGGAACTCTTTGGTCCATTTACAGCTTTGTACAGTCTGGGTGGAATCTCTCATATAC 631  
278 AAGTGTGCTATGGAATTTGCCAGCTTTTATAGGATGGCGCAAGCTTGATTTACT 337  
632 GCGTGGAGTACTGCTGTGATATCCCTGGCAATTTGGACGCTACATTTCTGGAACCAATTT 691  
338 TTCTGCTAATATGCTCAATTCGATATCTGTTT-----CGACACAAATTGA 385  
692 TTATTCATGTGAATCCCTGAACTTGGACCAAGCTCAATACAGCTGTGGGCATACTG 751  
386 CGAATCTTATACAAATTTCTACCGATTTATCTTTGTTGATTCAGTATCACCGCTGTT 445  
752 TAGTGATGGTCTTAATAGCATGAGTGTGAGTGGAGCGCCCGGATCCAGATTTTCTTAA 811  
446 CTGTGACAGGTTGAAATTTGTAGGACAAAGTCGGTCTCTGTACAATCAGTGAGCT 505  
812 CCTTTGCAAGCTCACAGCAATCTGTAATATAGTCCCTGGAGTATGAGCTAATTA 871  
506 TGATTTGTAATTAATACCAATTTGCTGTGATTTGTCATATGGGATTAATGCCCGAGAC 565  
872 AAGTCAAAACGACAACTTTAAAGACGCTTTTCAGGAGAGATTTCAAGTATTAACGGGT 931  
566 AAGCACTGCTCAGTTATTCATTCGAGCTGGAAAGATGTTACTTTTGTGCAAGGAT 625  
932 TGCCACTGGCTTTTATTATGAAATGATGCAATGCTGGGTGTTTAACTCACTTTG 991  
626 TGAGCAGTGGTGTGTAGCAAGTTGTTGCTTATGACGGCTGGTGTAGTGTGGTGCAA 685  
992 TTACTGAAGAGTAGAAGAACCTGAAAAACCAATTCCTGCAATATGTAATATCCATGG 1051  
686 TGGCAGCGGAATGAAACGGCGGAAAAAGATTTGCCATAAGCAATTTCTTGGTTGA 745  
1052 CCATTGTACCATTTGGCTATGCTGACAAATGTCGCTACTTTACGACCAATTAATGCTG 1111  
746 GTTTGTAAACAGTCGTTTATCTATTGATCAATTTTGTGTTTTTGGAAACTTTCGCCGATG 805

QY 1112 AGGAGCT---GCTGCTTTCAAATGCACTGGCAGTGAACCTTTTCTGAGCGGCTACTGGAA 1168  
DB 806 ATCATCTTGGCGGTAAATTTGAATGCAGCTTCTGAGCATCAGAGCTCAATTTTGGAGAA 865  
QY 1169 ATTTCTCATTAGCAGTTCCGATCTTTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1228  
DB 866 TCGGTGGAAGAGCTGGTCACTATTGGGATCTTGATCTCGGTATACGGTGCATTTGAACGGTT 925  
QY 1229 GTGTGTTTGTCTCTCCAGGTATTCTATGTTGGTCTGAGAGGGTCACTTTCCAGAA 1288  
DB 926 ATACACTAACTGGATCCGGTGCCTTATGCGATGGCTTTTAGAAGACGATCACTACCTTCA 985  
QY 1289 TCCTCTCCATGATTCATGTCGCGAAGCACACACTCTCTACAGCTGTATTGTTTTCACCC 1348  
DB 986 GTAAACAGCTGACAAATCTTTCAAGAGATTACGGTTCCTTATGTCCTGCGGTTTCC 1045  
QY 1349 CTTTGACAAAT-----GATAATGCTCTTCTGTGAGACCTCGACAGCTTTTGTGAATTTCC 1402  
DB 1046 AGTTAGCAGTAGCTTGTATTATGATGAGCCTTGGTCTTCTTCGACTTTTAAACACATGT 1105  
QY 1403 TCAGTTTTCGAGTGGCTTTTATTTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGAT 1462  
DB 1106 TGATTTTGTGATGGCTGCTTACCTTACTGATTTGATCGGTTCTCTATTATTAACA 1165  
QY 1463 ACAAATGCCAGATATGATCGCTCTTTTCAAGGTGCCACTGT 1504  
DB 1166 AAAAGCGCGGAATTGCCAGGTCATATCAAGTACCACATT 1207

## RESULT 8

US-08-232-463-14  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

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/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ CLONE: DTZDPT-Fls
US-08-232-463-14

Query Match          3.0%; Score 67.4; DB 1; Length 7218;
Best Local Similarity 2.1%; Pred. No. 4.7e-08;
Matches 8; Conservative 235; Mismatches 136; Indels 0; Gaps 0;

QY 1184 TTCGATCTTTGTCGCCCTCTCTGCTTTGGCTCCATGAACGGTGTGTGCTGTCT 1243
Db |||||: : : : : : : : : : : : : : : : : : : : : : : : : : : :
1060 TTGCGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1119
QY 1244 CAGAGTTATCTATGTTGGCTCGAGAGGCTCACCTTCCAGAAAPCCCTCATGATC 1303
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1120 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1179
QY 1304 ATGTCGCAAGCACACTCTCTACCACTGTATTGTTTGCACCCCTTTGACAATGATAA 1363
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1180 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1239
QY 1364 TGCTCTCTCTGAGACCTCGACAGTCTTTTGAATTCCTCAGTTTGCAGGTGCTTT 1423
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1240 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1299
QY 1424 TTATTGGGCTGGCAGTGTGCTGGCTGATTATCTTCGATACAAATGCCAGATATGCATC 1483
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1300 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1359
QY 1484 GTCTTTCAAGTGCCACTGTTCATCCAGCTGTGTTTCTTCATCAGCTCTTCATGG 1543
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1360 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1419
QY 1544 TTGCGCTTTCCCTCTATTC 1562
Db 1420 YYYYYYYYYYYYGTAC 1438

RESULT 9
US-09-800-960-3/c
; Sequence 3, Application US/09800960
; Patent No. 6387677
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001158
; CURRENT APPLICATION NUMBER: US/09/800,960
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 62804
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(62804)
; OTHER INFORMATION: n = A,T,C or G
US-09-800-960-3

Query Match          2.3%; Score 51.6; DB 4; Length 62804;
Best Local Similarity 70.4%; Pred. No. 0.0024;
Matches 69; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 23 CATGCCAGCTGGGTGACAGTGAGACTCTGTCTCAACACAGAAATTAAGGAAAAAAGAGA 82
Db |||||: : : : : : : : : : : : : : : : : : : : : : : : : : : :
43599 CACTCCAGCTGGGTGAGAGTGAGATCCGCTCTAAAAAAGAAAAAAGAAAAAAGAGA 43540
QY 83 AAGAAAAAGAGAGAGAGGAAATTCAGGCCCAATTGTGG 120
Db |||||: : : : : : : : : : : : : : : : : : : : : : : : : : : :
43539 AAGCAATCTTTTAAAGATATCATTTATAGGCAGCGTGG 43502
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RESULT 10
US-09-128-155-16
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match          2.2%; Score 50; DB 3; Length 152331;
Best Local Similarity 73.2%; Pred. No. 0.0098;
Matches 82; Conservative 0; Mismatches 20; Indels 10; Gaps 1;

QY 1 GGAGTTTCAAGTGACGACAGATCATG-----CCAGCTGGGTGACAGTGAGACTC 50
Db 151204 GGAGTTTCAAGTGACGACAGATCGTGCACCTGCACCTCCAGCTGGGTGACAGGAGACTC 151263
QY 51 TGCTTCAACAGAAATTAAGAAAAAGAAAAAGAAAAAGAAAAAGAGAGAGAGAA 102
Db 151264 GGTCTCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAA 151315

RESULT 11
US-09-801-876B-3/c
; Sequence 3, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 148567
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(148567)
; OTHER INFORMATION: n = A,T,C or G
US-09-801-876B-3

Query Match          2.2%; Score 48.6; DB 4; Length 148567;
Best Local Similarity 53.1%; Pred. No. 0.023;
Matches 129; Conservative 0; Mismatches 109; Indels 5; Gaps 1;

QY 1 GGAGTTTCAAGTGACGACAGATCATGCGCTGGGTGACAGACTGTGTCTTCAAC 60
Db 79560 GGAGTTTCAAGTGACGACAGATCATGCGCTGGGTGACAGACTGTGTCTTCAAC 79501
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QY 61 AGAATTAAGGAAAAAGGAAAGAAAGAAAGAGAGAGAGAAATCCAGGCC-----AAT 115  
Db 79500 TCTCTCAAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAA 79441  
QY 116 TGTGCGATAGATTTTATCAATCTCGGATTTTTCGATCTTTTTCATCACTGG 175  
Db 79440 GTTTCGTGATGATTTTTCACAGCTGGACCTTTGCGGATTTGCGGATTTTCATGTCAGTCAATCT 79381  
QY 176 ATTCAAGAAAGCCTGTGTGTCACCATCTCCAAAGGAGGTTTACCTGCAGGGAATGTTA 235  
Db 79380 ATACATCCACATCTTTGTAGTTTGTAAATTTGGTTAGATCTAGAGGCTTGTC 79321  
QY 236 ACG 238  
Db 79320 AAG 79318

RESULT 12  
US-09-691-861A-3/c  
; Sequence 3, Application US/09691861A  
; Patent No. 6482935  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: THEREOF  
; CURRENT APPLICATION NUMBER: US/09/691,861A  
; CURRENT FILING DATE: 2000-10-18  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 9862  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-691-861A-3

Query Match 2.1%; Score 47.4; DB 4; Length 9862;  
Best Local Similarity 70.8%; Pred. No. 0.013; 26; Indels 0; Gaps 0;  
Matches 63; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 23 CATCCAGCCTGGGTGACAGTGAGACTCTGCTCAACAGAAATTAAGGAAAAAGAAAGA 82  
Db 4055 CACTCCAGCCTGGGTGACAGTGAGACTCTGCTCAACAAAAAAGAAAAAAGAA 3996  
QY 83 AAGAAAAAGAGAGAGAGAAATTCAGGC 111  
Db 3995 AAGAAAAAAGACGCTAACAGTGTGGC 3967

RESULT 13  
US-09-876-216-3/c  
; Sequence 3, Application US/09876216  
; Patent No. 6544764  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN DEHYDROGENASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN DEHYDROGENASE  
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CL000906  
; CURRENT APPLICATION NUMBER: US/09/876,216  
; CURRENT FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 14485  
; TYPE: DNA  
; ORGANISM: Human  
US-09-876-216-3  
Query Match 2.1%; Score 46.8; DB 4; Length 14485;  
Best Local Similarity 63.2%; Pred. No. 0.023;

Matches 72; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
QY 23 CATCCAGCCTGGGTGACAGTGAGACTCTGCTCAACAGAAATTAAGGAAAAAGAAAGA 82  
Db 5077 CACTCCAGCCTGGGTGACAGTGAGACTCTGCTCTAAAAATATAAATGAATAAAAACGA 5018  
QY 83 AAGAAAAAGAGAGAGAGAAATTCAGGCCAAATTTGGCATAGATTTTATCATATA 136  
Db 5017 TATTAATATAAATAAGTAAATAACAGGGCAAGAGACATATAAATGAACAACA 4964

RESULT 14  
US-08-213-419B-3/c  
; Sequence 3, Application US/08213419B  
; Patent No. 6333406  
; GENERAL INFORMATION:  
; APPLICANT: Inselburg, J. et al.  
; TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: JII-002CNCIP  
; CURRENT APPLICATION NUMBER: US/08/213,419B  
; CURRENT FILING DATE: 1994-03-14  
; PRIOR APPLICATION NUMBER: US 07/870,506  
; PRIOR FILING DATE: 1992-04-17  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 6124  
; TYPE: DNA  
; ORGANISM: Plasmodium falciparum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2407)..(2439)  
; NAME/KEY: CDS  
; LOCATION: (2598)..(3404)  
; NAME/KEY: CDS  
; LOCATION: (3580)..(3720)  
; NAME/KEY: CDS  
; LOCATION: (3850)..(5835)  
US-08-213-419B-3

Query Match 2.0%; Score 44.8; DB 4; Length 6124;  
Best Local Similarity 53.4%; Pred. No. 0.054;  
Matches 94; Conservative 0; Mismatches 82; Indels 0; Gaps 0;  
QY 1788 ATTTTACTTCATTTTCTGAAAGTCTAGAGAAATTAACACTTTGGTGATAACAAAGAG 1847  
Db 2350 ATGTTTGATTTATTTAAATTTTCTTTATGTATAATATATGATTTTATAATATATAT 2291  
QY 1848 TCAGTTATTTTATTCATATATTTTACATATTCGAACATAATTTCTAAGAAATTTAGTTA 1907  
Db 2290 ATATTATTTTATTTTATTTTATTTTGGACATCTAAATTTAAATTTTAAATTTAAAAATTT 2231  
QY 1908 TAACTCTATGATGATAGAAAGTGAATATGCAATGTTTCTATGAGTCGCAATTT 1963  
Db 2230 ATTATATATATATATATAATTTTAAATATAATATATATATATATATTTTAAATTTATT 2175

RESULT 15  
US-09-803-671B-3/c  
; Sequence 3, Application US/09803671B  
; Patent No. 6582946  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: THEREOF  
; FILE REFERENCE: CL001161  
; CURRENT APPLICATION NUMBER: US/09/803,671B  
; CURRENT FILING DATE: 2001-03-12  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3

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; LENGTH: 64467
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(64467)
; OTHER INFORMATION: n = A,T,C or G
US-09-803-671B-3

Query Match      2.0%; Score 44.2; DB 4; Length 64467;
Best Local Similarity 71.8%; Pred. NO. 0.24;
Matches 58; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY      23 CATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAACACAGATTAAAGGAAAAAAGAGAGA 82
Db      20865 CACTCCAGCCTGGGTGACAGTGAGACCTCTCAAAAGAGAAAAAGAGAGAGAGA 20806

QY      83 AAGAAAAAGAGAGAGAGAAA 103
Db      20805 GAAAGAGAGAGAGAGAAAAA 20785

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Search completed: October 30, 2003, 07:16:01  
Job time : 124 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comput

OM nucleic - nucleic search, using sw model

Run on: October 30, 2003, 04:43:10 ; Search time 1053 Seconds  
(without alignments)  
5783.111 Million cell updates

Title: US-09-667-170A-440

Perfect score:

Sequence: 1 ggaggttgaagtgagcagag.....ttattaaaaaaaaaaaaaa 2239

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1811591 seqs, 1359896290 residues

Total number of hits satisfying chosen parameters: 3623182

Minimum DB seq length: 0

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%  
Maximum Match 100%

Maximum Macchi 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/prodata/2/pubnpa/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/prodata/2/pubnpa/PCT\_NEW PUB.seq.\*
- 3: /cgn2\_6/prodata/2/pubnpa/US06\_NEW PUB.seq.\*
- 4: /cgn2\_6/prodata/2/pubnpa/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/prodata/2/pubnpa/US07\_NEW PUB.seq.\*
- 6: /cgn2\_6/prodata/2/pubnpa/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/prodata/2/pubnpa/US08\_NEW PUB.seq.\*
- 8: /cgn2\_6/prodata/2/pubnpa/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/prodata/2/pubnpa/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/prodata/2/pubnpa/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/prodata/2/pubnpa/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/prodata/2/pubnpa/US09\_NEW PUB.seq.\*
- 13: /cgn2\_6/prodata/2/pubnpa/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/prodata/2/pubnpa/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/prodata/2/pubnpa/US10\_NEW PUB.seq.\*
- 16: /cgn2\_6/prodata/2/pubnpa/US60\_NEW PUB.seq.\*
- 17: /cgn2\_6/prodata/2/pubnpa/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2239	100.0	2239	10	US-09-738-973-440	Sequence 440, App
2	2239	100.0	2239	10	US-09-954-133-440	Sequence 440, App
3	2239	100.0	2239	14	US-10-144-649A-740	Sequence 740, App
4	2082.8	93.0	6080	14	US-10-144-649A-740	Sequence 740, App
5	2080.8	92.9	5981	10	US-09-738-973-441	Sequence 441, App
6	2080.8	92.9	5981	10	US-09-954-133-441	Sequence 441, App
7	2080.8	92.9	5981	14	US-10-144-649A-441	Sequence 441, App
8	1900.2	84.3	3144	14	US-10-163-866-31	Sequence 31, Appl
9	1888.2	84.3	2482	14	US-10-163-866-29	Sequence 29, Appl
10	1715	76.6	2041	12	US-10-133-013-40	Sequence 40, Appl
11	1715	76.6	2041	12	US-10-247-671-78	Sequence 78, Appl
12	1540.8	68.8	1861	14	US-10-163-866-30	Sequence 30, Appl
13	1454.4	65.0	1542	14	US-10-163-866-33	Sequence 33, Appl
14	1431.8	63.9	1528	14	US-10-163-866-52	Sequence 52, Appl
15	1373.4	61.3	2000	14	US-10-163-866-34	Sequence 34, Appl
16	1047.4	46.8	1268	14	US-10-163-866-53	Sequence 53, Appl

## ALIGNMENTS

## RESULT 1

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US-09-738-973-440
/ Sequence 440, Application US/09738973
/ Patent No. US20020110563A1
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Fling, Steven P.
/ APPLICANT: Mohamath, Raodoh
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Secrist, Heather
/ APPLICANT: Indrias, Carol Yoseph
/ APPLICANT: Benson, Darin R.
/ APPLICANT: Elliott, Mark
/ APPLICANT: Mannion, Jane
/ APPLICANT: Kalos, Michael D.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
/ TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF
/ FILE REFERENCE: 210121-47509
/ CURRENT APPLICATION NUMBER: US/09/738,973
/ CURRENT FILING DATE: 2000-12-14
/ NUMBER OF SEQ ID NOS: 587
/ SOFTWARE: Fast-Seq for Windows Version 3.0
/ SEQ ID NO 440
/ LENGTH: 2239
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-738-973-440

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Query Match 100.0%; Score 2239; DB 10; Length 2239;  
Best Local Similarity 100.0%; Pred. No. 0;

QY 1 GGAGGTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGAGTGAGACTCTGTCTCAAC 60

Db 1 GGAGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAC 60

QY 61 AGAATTAAGGAAAAAGAAAGAAAGAGAGAGAGGAAATTCACGGCCAAATTGTGG 120

Db 61 AGAATTAAGGAAAAAGAAAAAGAAAAAGAGAGAGAAATTCAGGCCAATTTGTGG 120  
QY 121 CATAGATTTTATCATATCTCGATTTTGTGATTTTGGATTTCTTTGTTCTCATCATCTGGATTCA 180  
Db 121 CATAGATTTTATCATATCTCGATTTTGTGATTTTGGATTTCTTTGTTCTCATCATCTGGATTCA 180  
QY 181 GGAAGCCGTGTTGTGTCACCATCTCCAAAGGAGTTTACCTGACGGGAAATGTTAACGGG 240  
Db 181 GGAAGCCGTGTTGTGTCACCATCTCCAAAGGAGTTTACCTGACGGGAAATGTTAACGGG 240  
QY 241 AGCTGCTTCCCTGGGCAACAGAGGCCACCTGGGCGAGAGCCCTTTTCAGGAAAGAGAC 300  
Db 241 AGCTGCTTCCCTGGGCAACAGAGGCCACCTGGGCGAGAGCCCTTTTCAGGAAAGAGAC 300  
QY 301 GCCTTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTCAGCTGAGAGGAAAGTC 360  
Db 301 GCCTTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTCAGCTGAGAGGAAAGTC 360  
QY 361 ACTTTACTGAGGGAGTCTCCATTTATCATTTGGCACCATTATGGACAGGAATCTTCATC 420  
Db 361 ACTTTACTGAGGGAGTCTCCATTTATCATTTGGCACCATTATGGACAGGAATCTTCATC 420  
QY 421 TCTCCTAAGGGCGTCTCAGAACACGGCGACGGTGGGCATGTCCTGACCAATCTGGACG 480  
Db 421 TCTCCTAAGGGCGTCTCAGAACACGGCGACGGTGGGCATGTCCTGACCAATCTGGACG 480  
QY 481 GTGTGTGGGTCCTGTCATTTATTTGGAGCTTTGTCTTATGCTGAAATTTGGGAAACAATA 540  
Db 481 GTGTGTGGGTCCTGTCATTTATTTGGAGCTTTGTCTTATGCTGAAATTTGGGAAACAATA 540  
QY 541 AAGAAATCTGGAGGTCATTACACATATTTTGGAGTCTTTGGTCCATTACACAGCTTTT 600  
Db 541 AAGAAATCTGGAGGTCATTACACATATTTTGGAGTCTTTGGTCCATTACACAGCTTTT 600  
QY 601 GTACGAGTCTGGGTGGAATCTCTATATACGCCCTGCGAGCTACTGCTGTGATATCCCTG 660  
Db 601 GTACGAGTCTGGGTGGAATCTCTATATACGCCCTGCGAGCTACTGCTGTGATATCCCTG 660  
QY 661 GCATTTGACCGCTACATTTCTGAAACCATTTTATTTCAATGGAATCCCTGAACTGGC 720  
Db 661 GCATTTGACCGCTACATTTCTGAAACCATTTTATTTCAATGGAATCCCTGAACTGGC 720  
QY 721 ATCAAGCTCATTAAGCTGTGGGCATACTGTAGTGATGGTCTCTAAATAGCATGAGTCTC 780  
Db 721 ATCAAGCTCATTAAGCTGTGGGCATACTGTAGTGATGGTCTCTAAATAGCATGAGTCTC 780  
QY 781 AGCTGAGCGCCGGATCCAGATTTCTTAACCTTTTGAAGCTCACAGCAATCTGTATA 840  
Db 781 AGCTGAGCGCCGGATCCAGATTTCTTAACCTTTTGAAGCTCACAGCAATCTGTATA 840  
QY 841 ATTAAGTCCCTGGAGTATGAGCTAATTAAGGTCAAACGAGAACTTTAAGACGCC 900  
Db 841 ATTAAGTCCCTGGAGTATGAGCTAATTAAGGTCAAACGAGAACTTTAAGACGCC 900  
QY 901 TTTTCAGGAAGAGATCAAGTATTAAGGTTTGGCTGGCTTTTATTAAGGAATGAT 960  
Db 901 TTTTCAGGAAGAGATCAAGTATTAAGGTTTGGCTGGCTTTTATTAAGGAATGAT 960  
QY 961 GCATATGCTGGCTGGTTTACCTCACTTTGTACTGGAAGATGAGAAACCTGAAAAA 1020  
Db 961 GCATATGCTGGCTGGTTTACCTCACTTTGTACTGGAAGATGAGAAACCTGAAAAA 1020  
QY 1021 ACCATTCCCTTSCAATATGATATCCATGGCAATTTGACCATTTGGCTATGTCGTGACA 1080  
Db 1021 ACCATTCCCTTSCAATATGATATATCCATGGCAATTTGACCATTTGGCTATGTCGTGACA 1080  
QY 1081 AATGGGCTACTTTACGACCAATTAATGCTGAGGAGCTGCTCTTTCAATGCGAGTGCA 1140  
Db 1081 AATGGGCTACTTTACGACCAATTAATGCTGAGGAGCTGCTCTTTCAATGCGAGTGCA 1140  
QY 1141 GTGACCTTTCTGACGGCTACTGGAAATTTCTCATTAGCAGTTCCGATCTTTGTGCCC 1200  
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Db 1141 GTGACCTTTCTGACGGCTACTGGAAATTTCTCATTAGCAGTTCCGATCTTTGTGCCC 1200  
QY 1201 CTCTCCTGCTTTGGCTCTCATGAACGGTGGTGTGTTTGTCTCCAGGTTATTTCTATGTT 1260  
Db 1201 CTCTCCTGCTTTGGCTCTCATGAACGGTGGTGTGTTTGTCTCCAGGTTATTTCTATGTT 1260  
QY 1261 GGGTCTCGAGAGGGTCACCTTCCAGAAATCTCTCCATGATTCATGTCGGAAGACACT 1320  
Db 1261 GGGTCTCGAGAGGGTCACCTTCCAGAAATCTCTCCATGATTCATGTCGGAAGACACT 1320  
QY 1321 CCTTACACAGCTGTTATTTGTTTTCACCCCTTTGACAAATGATAATCTCTTCTCTCGAGAC 1380  
Db 1321 CCTTACACAGCTGTTATTTGTTTTCACCCCTTTGACAAATGATAATCTCTTCTCGAGAC 1380  
QY 1381 CTCGACGCTTTTGAATTTCTCAGTTTTCAGGTTGGCTTTTATTTGGCTGGCAGTT 1440  
Db 1381 CTCGACGCTTTTGAATTTCTCAGTTTTCAGGTTGGCTTTTATTTGGCTGGCAGTT 1440  
QY 1441 GCTGGCTGATTTATCTTCGATACAAATGCCCAGATATGTCCTTCAAGGTGCA 1500  
Db 1441 GCTGGCTGATTTATCTTCGATACAAATGCCCAGATATGTCCTTCAAGGTGCA 1500  
QY 1501 CTGTTCACTCCAGCTTTCTTTTCTTCATGCTCTTTCATGTTGCCCTTTCCCTCTAT 1560  
Db 1501 CTGTTCACTCCAGCTTTCTTTTCTTCATGCTCTTTCATGTTGCCCTTTCCCTCTAT 1560  
QY 1561 TCGACCCATTTAGTACAGGATTTGGCTTCTGTCATCTGACCTGAGTCCCTGCGTAT 1620  
Db 1561 TCGACCCATTTAGTACAGGATTTGGCTTCTGTCATCTGACCTGAGTCCCTGCGTAT 1620  
QY 1621 TATCTCTTTATATATGAGCAAGAAACCCAGGTGTTTGAATAATCTCAGAGAAATA 1680  
Db 1621 TATCTCTTTATATATGAGCAAGAAACCCAGGTGTTTGAATAATCTCAGAGAAATA 1680  
QY 1681 ACCAGAACATTTACAAATAATCTGGAAGTTCTACAGAGAGAGTAAGTTATGACTAAT 1740  
Db 1681 ACCAGAACATTTACAAATAATCTGGAAGTTCTACAGAGAGAGTAAGTTATGACTAAT 1740  
QY 1741 GGACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAATATGGGATTTTACTTCAAT 1800  
Db 1741 GGACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAATATGGGATTTTACTTCAAT 1800  
QY 1801 TTTCTGAAGTCTAGAGAAATTAACAATTTGTTGATATAACAAAGAGGTCAGTTATTTTA 1860  
Db 1801 TTTCTGAAGTCTAGAGAAATTAACAATTTGTTGATATAACAAAGAGGTCAGTTATTTTA 1860  
QY 1861 TTTCTATATTTTACATATTCGAATTAATTTCTAAGAAATTTAGTTATACTCTATGTAG 1920  
Db 1861 TTTCTATATTTTACATATTCGAATTAATTTCTAAGAAATTTAGTTATACTCTATGTAG 1920  
QY 1921 TTATAGAAAGTGAATATGCAATTTCTATGAGTCCGACAAATTTCTGAGTCTCTGATACC 1980  
Db 1921 TTATAGAAAGTGAATATGCAATTTCTATGAGTCCGACAAATTTCTGAGTCTCTGATACC 1980  
QY 1981 TACCTATTTGGGTTAGAGAAAGACTAGACAAATTAATGTTGTCATTTCTTCAACAT 2040  
Db 1981 TACCTATTTGGGTTAGAGAAAGACTAGACAAATTAATGTTGTCATTTCTTCAACAT 2040  
QY 2041 ATGTTAGCAGCGCAAGAAACCTTCAAAATGAGACTGAGATTTTCTGTATATATGGGTT 2100  
Db 2041 ATGTTAGCAGCGCAAGAAACCTTCAAAATGAGACTGAGATTTTCTGTATATATGGGTT 2100  
QY 2101 TTGTAAAGATGGTTTTACACACTACAGATCTCTATCTGTGAAAAGTGTCTCAATCTG 2160  
Db 2101 TTGTAAAGATGGTTTTACACACTACAGATCTCTATCTGTGAAAAGTGTCTCAATCTG 2160  
QY 2161 AAAAAACCATACATCATGATTTATGGCAAGAGAGAGAGGTAGAGCTGTCTTTAAT 2220  
Db 2161 AAAAAACCATACATCATGATTTATGGCAAGAGAGAGAGGTAGAGCTGTCTTTAAT 2220  
QY 2221 TATTAAAAAATAAAAAA 2239  
Db 2221 TATTAAAAAATAAAAAA 2239



RESULT 2  
US-09-854-133-440  
; Sequence 440, Application US/09854133  
; Publication No. US20020183499A1  
; GENERAL INFORMATION:  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Mohamath, Raodoh  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.475C10  
; CURRENT APPLICATION NUMBER: US/09/854,133  
; CURRENT FILING DATE: 2001-05-11  
; NUMBER OF SEQ ID NOS: 735  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 440  
; LENGTH: 2239  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-854-133-440

Query Match 100.0%; Score 2239; DB 10; Length 2239;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGAGGTTGAAGTGACGAGATCATGCCAGCTGGGTGACGTGAGACTCTCTCAAAAC	60
DB	1	GGAGGTTGAAGTGACGAGATCATGCCAGCTGGGTGACGTGAGACTCTCTCAAAAC	60
QY	61	AGAAATTAAGGAAAGAAAGAAAGAAAGAAAGAGAGAGAGAAATCCAGGCCAAATGTGG	120
DB	61	AGAAATTAAGGAAAGAAAGAAAGAAAGAAAGAGAGAGAGAAATCCAGGCCAAATGTGG	120
QY	121	CATGATTTTATCATATTCTGGATTTTGTGGATTTCTTTTGTCTCATCTGATTCATCA	180
DB	121	CATGATTTTATCATATTCTGGATTTTGTGGATTTCTTTTGTCTCATCTGATTCATCA	180
QY	181	GGAAAGCCCTGTTGTGTCACCATCTCCAAAGAGAGTTACCTGAGGAAATGTTAACGGG	240
DB	181	GGAAAGCCCTGTTGTGTCACCATCTCCAAAGAGAGTTACCTGAGGAAATGTTAACGGG	240
QY	241	AGGCTGCTTCCCTGGGCAACAGAGAGCCACCTGGGAGAGCCCTGGGAGAGAGAGAC	300
DB	241	AGGCTGCTTCCCTGGGCAACAGAGAGCCACCTGGGAGAGAGAGAC	300
QY	301	GCCTTTTCAGGAAGAGACGCTTTTCAGGAAGAGAGAGAGAGAGAGAGAGAGAGAC	360
DB	301	GCCTTTTCAGGAAGAC	360
QY	361	ACTTTTACTGAGGAGAGTCTCATATCATTTGTCACCATCATTTGAGAGAGAGAGAG	420
DB	361	ACTTTTACTGAGGAGAGTCTCATATCATTTGTCACCATCATTTGAGAGAGAGAGAG	420
QY	421	TCTCTAAGGCGTCTCCAGAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	480
DB	421	TCTCTAAGGCGTCTCCAGAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	480
QY	481	GTGTGTGGGCTCTGTCTCATATTTGGAGCTTTGTCTATGCTGAAATGGGAGAGAG	540
DB	481	GTGTGTGGGCTCTGTCTCATATTTGGAGCTTTGTCTATGCTGAAATGGGAGAGAG	540
QY	541	AAGAAATCTGAGGAGTCTATACATATATTTTGAAGTCTTTTGGTCCATACAGCTTTT	600
DB	541	AAGAAATCTGAGGAGTCTATACATATATTTTGAAGTCTTTTGGTCCATACAGCTTTT	600
QY	601	GTACGAGTCTGGGTGGAACTCCTCATATATAGCCCTGAGCTACTGCTGTGATTCCTG	660
DB	601	GTACGAGTCTGGGTGGAACTCCTCATATATAGCCCTGAGCTACTGCTGTGATTCCTG	660

QY	661	GCATTTGGAGCGCTACATCTCTGGAAACCATTTTATTCATGTGAATCCCTGAACCTTGG	720
DB	661	GCATTTGGAGCGCTACATCTCTGGAAACCATTTTATTCATGTGAATCCCTGAACCTTGG	720
QY	721	ATCAAGCTCATTTACAGCTGTGGGCATAACTGTAGTGAATCTTAAATAGCAATGATGTC	780
DB	721	ATCAAGCTCATTTACAGCTGTGGGCATAACTGTAGTGAATCTTAAATAGCAATGATGTC	780
QY	781	AGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTGCAAGCTCACAGCAATTCGTATA	840
DB	781	AGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTGCAAGCTCACAGCAATTCGTATA	840
QY	841	ATTATAGTCCCTGGAGTTATGAGCTTAATTAAGGTCAAACCGCAACTTTTAAAGCGCC	900
DB	841	ATTATAGTCCCTGGAGTTATGAGCTTAATTAAGGTCAAACCGCAACTTTTAAAGCGCC	900
QY	901	TTTTTCAGGAAGAGATTCAAGTATTACGGGTTGCGGCTTTTATTTATGGAATGTAT	960
DB	901	TTTTTCAGGAAGAGATTCAAGTATTACGGGTTGCGGCTTTTATTTATGGAATGTAT	960
QY	961	GCATATGCTGGCTGTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCCTGAAAA	1020
DB	961	GCATATGCTGGCTGTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCCTGAAAA	1020
QY	1021	ACCATTCCCTTGCATATATGATATATCCATGTCATTTGTCATTTGCTGCTGCTGACA	1080
DB	1021	ACCATTCCCTTGCATATATGATATATCCATGTCATTTGTCATTTGCTGCTGCTGACA	1080
QY	1081	AATGTGGCTACTTTACGACCAATTAATCTGAGGAGCTGCTGCTTCAAAATGCACTGGCA	1140
DB	1081	AATGTGGCTACTTTACGACCAATTAATCTGAGGAGCTGCTGCTTCAAAATGCACTGGCA	1140
QY	1141	GTGACCTTTTCTGAGCGGCTACTGCGAAATTTCTCAATAGCAGTTCCGATCTTTGTTGCC	1200
DB	1141	GTGACCTTTTCTGAGCGGCTACTGCGAAATTTCTCAATAGCAGTTCCGATCTTTGTTGCC	1200
QY	1201	CTCTCTGCTTGGCTCCATGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1260
DB	1201	CTCTCTGCTTGGCTCCATGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1260
QY	1261	GCCTCTGAGAGGCTACCTTCCAGAAATCTCTCCATGATTCATGTCGCAAGCAGCACT	1320
DB	1261	GCCTCTGAGAGGCTACCTTCCAGAAATCTCTCCATGATTCATGTCGCAAGCAGCACT	1320
QY	1321	CCTCTACAGCTGTTATTTGTTGCAACCTTTGCAATGATGATGCTCTCTCTGAGAGAC	1380
DB	1321	CCTCTACAGCTGTTATTTGTTGCAACCTTTGCAATGATGATGCTCTCTCTGAGAGAC	1380
QY	1381	CTGACAGCTCTTTTGAATTTTCTCAGTTTTCAGAGTGGCTTTTATTTGGGCTGGCAGTT	1440
DB	1381	CTGACAGCTCTTTTGAATTTTCTCAGTTTTCAGAGTGGCTTTTATTTGGGCTGGCAGTT	1440
QY	1441	GCTGGGCTGATTTATCTTCGATAAAATGCGCAGATATGATCGCTCTTCAAGGTGCA	1500
DB	1441	GCTGGGCTGATTTATCTTCGATAAAATGCGCAGATATGATCGCTCTTCAAGGTGCA	1500
QY	1501	CTGTTTCAATCCAGCTTTGTTTCTCAGATGCTCTTCAATGCTGCTGCTGCTGCTGCTGCT	1560
DB	1501	CTGTTTCAATCCAGCTTTGTTTCTCAGATGCTCTTCAATGCTGCTGCTGCTGCTGCTGCT	1560
QY	1561	TCGAGACCATTTAGTACAGGATTTGGCTTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCT	1620
DB	1561	TCGAGACCATTTAGTACAGGATTTGGCTTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCT	1620
QY	1621	TATCTCTTTATTTATGCGGCAAGAAACCCAGTGGTGTGTAATTAATGTCAGAGAAATA	1680
DB	1621	TATCTCTTTATTTATGCGGCAAGAAACCCAGTGGTGTGTAATTAATGTCAGAGAAATA	1680
QY	1681	ACCAGAACTTACAAATATATGGAAGTGTACAGAGAGAGATTAAGTTATGAACCTAAT	1740
DB	1681	ACCAGAACTTACAAATATATGGAAGTGTACAGAGAGAGATTAAGTTATGAACCTAAT	1740
QY	1741	GGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAAATAGGATTTTACTTCAT	1800

Db	1741	GGACTTGAGATCTTGGCAATCTGCCAAGGGGAGACAAAAATAGGATTTTACTTTCAT	1800
Qy	1801	TTTCTGAAAGCTAGAGAAATPACAACTTTTGGTGATAACAAAAGAGCTCAGTATATTTTA	1860
Db	1801	TTTCTGAAAGCTAGAGAAATPACAACTTTTGGTGATAACAAAAGAGCTCAGTATATTTTA	1860
Qy	1861	TTCATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATACTCTATCTAG	1920
Db	1861	TTCATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATACTCTATCTAG	1920
Qy	1921	TTATAGAAAGTGAATATGCACTTATCTATGAGTCGCACAATTTCTTGAGTCTCTGATACC	1980
Db	1921	TTATAGAAAGTGAATATGCACTTATCTATGAGTCGCACAATTTCTTGAGTCTCTGATACC	1980
Qy	1981	TACCTATTTGGGGTTTAGAGAAAAGACTAGACAAATTAATCTATGCTGCTCATTCTCTACAACAT	2040
Db	1981	TACCTATTTGGGGTTTAGAGAAAAGACTAGACAAATTAATCTATGCTGCTCATTCTCTACAACAT	2040
Qy	2041	ATGTTAGCAGCGCAAGAACCTTCAAATTTGAAGACTGAGATTTTTCTGTGATATATATGGGTT	2100
Db	2041	ATGTTAGCAGCGCAAGAACCTTCAAATTTGAAGACTGAGATTTTTCTGTGATATATATGGGTT	2100
Qy	2101	TTGTTAAAGATGGTTTTACACACTACAGATGTCATATACTGTGAAAAGTGTTTTCAATTCGT	2160
Db	2101	TTGTTAAAGATGGTTTTACACACTACAGATGTCATATACTGTGAAAAGTGTTTTCAATTCGT	2160
Qy	2161	AAAAAAGCATACATCATGATTATGGCAAGAGAGAGAGGTAGAGCTGTTCTTAAATTT	2220
Db	2161	AAAAAAGCATACATCATGATTATGGCAAGAGAGAGAGGTAGAGCTGTTCTTAAATTT	2220
Qy	2221	TATTTAAAAAATAAAAAA 2239	
Db	2221	TATTTAAAAAATAAAAAA 2239	

### RESULT 3

```

US/10/144-649A-440
; Sequence 440, Application US/10144649A
; Publication NO. US20030118599A1
GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Aigace, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND PREVENTION OF HIV INFECTION
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144-649A-440
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSeq for Windows Version 1.0.0
; SEQ ID NO 440
; LENGTH: 2239
; TYPE: DNA
; ORGANISM: Homo sapiens
US/10/144-649A-440

```

	Query Match	100.0%;	Score 2239;	DB 14;	Length 2239;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
	Matches 2239;	Conservative	0;	Mismatches	0;	Gaps 0;
QY	1	GGAGGTTGAGTGACGACGAGATCATGCCAGCCTGGTGACAGTGCAGACTGTGTCCTCAAC	60			
Db	1	GGAGGTTCAAGTTCGACGACGAGATCATGCCAGCCTGGTGACAGTGCAGACTGTGTCCTCAAC	60			
QY	61	AGATTTAAGGAAAAAAGAAAGAAAAAGAGAGAGAGGAAATTCAGGCGCAATTGTGG	120			
Db	61	AGATTTAAGGAAAAAAGAAAGAAAAAGAGAGAGAGGAAATTCAGGCGCAATTGTGG	120			
QY	121	CATAGATTTTATCATATCTCGATTTTTCGATTTCTGTTTCTCATCTCGGATTC	180			

Db	121	CATAGATTTATCAATATCTCGAATTTTGGATTTCTTTTGTTTCTCATCACTGGATTCA	180
QY	181	GGAAAGCCTGTTGTCTCACCAATCTCCAAAGAGAGGTACCTGCGAGGAAATGTTTAACGG	240
Db	181	GGAAAGCCTGTTGTCTCACCAATCTCCAAAGAGAGGTACCTGCGAGGAAATGTTTAACGG	240
QY	241	AGGCTGCCTTCCCTGGGCAACAAGGAGCCACTGGCGAGGACGCCCTTTTCAGGAAGAGAC	300
Db	241	AGGCTGCCTTCCCTGGGCAACAAGGAGCCACTGGCGAGGACGCCCTTTTCAGGAAGAGAC	300
QY	301	GCCTTTTCAGGAAGAGAGCGCCTTTTCAGRAAGAGAAAGTGCAGCTCAAGAGGAAATC	360
Db	301	GCCTTTTCAGGAAGAGAGCGCCTTTTCAGRAAGAGAAAGTGCAGCTCAAGAGGAAATC	360
QY	361	ACTTTACTGAGGGAGTCTCCATTATCATTCGCAACCATCATTTGGAGCAGGAAATCTTCATC	420
Db	361	ACTTTACTGAGGGAGTCTCCATTATCATTCGCAACCATCATTTGGAGCAGGAAATCTTCATC	420
QY	421	TCTCCTAAGGCGTGCTCCAGAACACGGGCGAGCGTGGGCATGTCTCTGACCATCTGGACG	480
Db	421	TCTCCTAAGGCGTGCTCCAGAACACGGGCGAGCGTGGGCATGTCTCTGACCATCTGGACG	480
QY	481	GTGCTGTGGGTCCTGTCTCACTATTTTGGAGCTTTGTCTTATGCTGAATTTGGGAACTATA	540
Db	481	GTGCTGTGGGTCCTGTCTCACTATTTTGGAGCTTTGTCTTATGCTGAATTTGGGAACTATA	540
QY	541	AAGAAATCTGGAGGTCATTACACATATATTTTGGAAAGTCTTTGTTCANTTACCAGCTTTT	600
Db	541	AAGAAATCTGGAGGTCATTACACATATATTTTGGAAAGTCTTTGTTCANTTACCAGCTTTT	600
QY	601	GTACGAGTCTGGTGGAACTCCTCATAAATACGCCCTCGAGCTACTGCTGTGATATCCCTG	660
Db	601	GTACGAGTCTGGTGGAACTCCTCATAAATACGCCCTCGAGCTACTGCTGTGATATCCCTG	660
QY	661	GCATTTGGACGCTACATTTCTGGAAACCATTTTTTATTTCAATGTGAAATCCCTGAATTCGC	720
Db	661	GCATTTGGACGCTACATTTCTGGAAACCATTTTTTATTTCAATGTGAAATCCCTGAATTCGC	720
QY	721	ATCAAGCTCATTAACAGCTGTGGGCATAACTAGTGTATGGTCCCTAAATAGCATGAGTGC	780
Db	721	ATCAAGCTCATTAACAGCTGTGGGCATAACTAGTGTATGGTCCCTAAATAGCATGAGTGC	780
QY	781	AGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAGCTTCAGACAAATCTGATA	840
Db	781	AGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAGCTTCAGACAAATCTGATA	840
QY	841	ATTATAGTCCCTGGAGTTATGCACTAATTAAGGTCARAACGAGAACTTTTAAAGACGCC	900
Db	841	ATTATAGTCCCTGGAGTTATGCACTAATTAAGGTCARAACGAGAACTTTTAAAGACGCC	900
QY	901	TTTTCAGGAAGAGATTCAGATTTATACCGGTTTGCCACTGGCTTTTATATGGAATGTAT	960
Db	901	TTTTCAGGAAGAGATTCAGATTTATACCGGTTTGCCACTGGCTTTTATATGGAATGTAT	960
QY	961	GCATATGCTGGCTGTTTTTACCTCAAATTTGTGTTACTGAAGAAGTAGAAAAACCCCTGAAAA	1020
Db	961	GCATATGCTGGCTGTTTTTACCTCAAATTTGTGTTACTGAAGAAGTAGAAAAACCCCTGAAAA	1020
QY	1021	ACCAATCCCTTGCAATATGATATCATGGCCATGTCTACCACTGGCTATGCTGACAC	1080
Db	1021	ACCAATCCCTTGCAATATGATATCATGGCCATGTCTACCACTGGCTATGCTGACAC	1080
QY	1081	AATGTGCGCTACTTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTTCAAAATGAGTGGCA	1140
Db	1081	AATGTGCGCTACTTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTTCAAAATGAGTGGCA	1140
QY	1141	GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCAATAGCAGTCCGATCTTTGTGCC	1200
Db	1141	GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCAATAGCAGTCCGATCTTTGTGCC	1200
QY	1201	CTCTCCTGCTTTGGCTCCATGAACGGTGTGTGTGTCTGCTCTCCAGGTATTTCTATGTT	1260
Db	1201	CTCTCCTGCTTTGGCTCCATGAACGGTGTGTGTGTGTCTGCTCTCCAGGTATTTCTATGTT	1260

Qy	1261	GC	GCTCTCGAGAGGGT	CACCTTCCAGAAATCCTCTCCATGATTTCATGTCGCGAAGCACACT	1320
Db	1261	GC	GCTCTCGAGAGGGT	CACCTTCCAGAAATCCTCTCCATGATTTCATGTCGCGAAGCACACT	1320
Qy	1321	CC	TCTACCAAGCTGTAT	TGTTTGGCACCCCTTTGGCAATATGCTTCTCTCTGGAAGAC	1380
Db	1321	CC	TCTACCAAGCTGTAT	TGTTTGGCACCCCTTTGGCAATATGCTTCTCTCTGGAAGAC	1380
Qy	1381	CT	GACAGTCTTTTGAATTT	CCTCAGTTTGGCCAGGTGGCTTTTATTTGGCTGGCGACTT	1440
Db	1381	CT	GACAGTCTTTTGAATTT	CCTCAGTTTGGCCAGGTGGCTTTTATTTGGCTGGCGACTT	1440
Qy	1441	GCT	GGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCTTTCAAGTGCCA	1500	
Db	1441	GCT	GGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCTTTCAAGTGCCA	1500	
Qy	1501	CT	GTTTCATCCCAAGCTTTGTTTTCCTTCACATGCTCTTCATGGTTGCCCTTCCCTCTAT	1560	
Db	1501	CT	GTTTCATCCCAAGCTTTGTTTTCCTTCACATGCTCTTCATGGTTGCCCTTCCCTCTAT	1560	
Qy	1561	TC	GGACCCATTTAGTACAGGATTTGGCTTCGTTCATCACTCTGACTGGAGTCCCTGCGTAT	1620	
Db	1561	TC	GGACCCATTTAGTACAGGATTTGGCTTCGTTCATCACTCTGACTGGAGTCCCTGCGTAT	1620	
Qy	1621	TAT	CTCTTTTATATATGGGCAAGAAACCCAGGTGGTTTGAATAATATGTCAGAGAAAATA	1680	
Db	1621	TAT	CTCTTTTATATATGGGCAAGAAACCCAGGTGGTTTGAATAATATGTCAGAGAAAATA	1680	
Qy	1681	ACC	AGAACATTCACAAATAATACGTGAAGTTGTACCAAGAGAAGATAGTTATGACTAAT	1740	
Db	1681	ACC	AGAACATTCACAAATAATACGTGAAGTTGTACCAAGAGAAGATAGTTATGACTAAT	1740	
Qy	1741	GG	ACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAATAGGGATTTTACTTTCAT	1800	
Db	1741	GG	ACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAATAGGGATTTTACTTTCAT	1800	
Qy	1801	TT	CTGGAAGCTCTAGAGAATTCACATTTGGTGATTAACAAAAGGAGTCAAGTTATTTTA	1860	
Db	1801	TT	CTGGAAGCTCTAGAGAATTCACATTTGGTGATTAACAAAAGGAGTCAAGTTATTTTA	1860	
Qy	1861	TT	CATATTTTATAGCATATTCGAACATAATTTCTAAGAAATTTAGTTATTAACCTATGTTAG	1920	
Db	1861	TT	CATATTTTATAGCATATTCGAACATAATTTCTAAGAAATTTAGTTATTAACCTATGTTAG	1920	
Qy	1921	TT	ATAGAAAGTGAATATGCAATTTCTATGAGTCGCACAATTTCTGAGTCTCTGATACC	1980	
Db	1921	TT	ATAGAAAGTGAATATGCAATTTCTATGAGTCGCACAATTTCTGAGTCTCTGATACC	1980	
Qy	1981	TAC	CTATTTGGGTTAGAGAAAAGCTAGACAAATTTCTATGAGTGGTCACTTCTCAACAT	2040	
Db	1981	TAC	CTATTTGGGTTAGAGAAAAGCTAGACAAATTTCTATGAGTGGTCACTTCTCAACAT	2040	
Qy	2041	AT	GTTAGCGGCAAGAAACCTTCAAATTTGAAGACTGAGATTTTTCTGTATATATGCGTT	2100	
Db	2041	AT	GTTAGCGGCAAGAAACCTTCAAATTTGAAGACTGAGATTTTTCTGTATATATGCGTT	2100	
Qy	2101	TT	GTAAGATGGTTTACACACTACAGATGCTATATCTGTGAAAAGTGTTTTCAATTCG	2160	
Db	2101	TT	GTAAGATGGTTTACACACTACAGATGCTATATCTGTGAAAAGTGTTTTCAATTCG	2160	
Qy	2161	AAAA	AAAGCATACATCATGATTATGGCAAGAGGAGAGAGGTAGAGCTGTCTTAAAT	2220	
Db	2161	AAAA	AAAGCATACATCATGATTATGGCAAGAGGAGAGAGGTAGAGCTGTCTTAAAT	2220	
Qy	2221	TAT	TAAAAAATAAAAAA	2239	
Db	2221	TAT	TAAAAAATAAAAAA	2239	

RESULT 4  
US-10-144-649A-740  
; Sequence 740, Application US/101444649A

; Publication No. US20030118599A1									
; GENERAL INFORMATION:									
; APPLICANT: Lodges, Michael J.									
; APPLICANT: wang, Tongtong									
; APPLICANT: Fan, Liqun									
; APPLICANT: Algate, Paul A.									
; APPLICANT: McNeill, Patricia D.									
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR									
; FILE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER									
; FILE REFERENCE: 210121.475C11									
; CURRENT APPLICATION NUMBER: US/10/144,649A									
; CURRENT FILING DATE: 2002-08-21									
; NUMBER OF SEQ ID NOS: 749									
; SOFTWARE: FastSeq for Windows Version 3.0									
; SEQ ID NO 740									
; LENGTH: 6080									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-144-649A-740									
Query Match	93.0%;	Score 2082.8;	DB 14;	Length 6080;					
Best Local Similarity	97.5%;	Pred. No. 0;							
Matches 2148;	Conservative 0;	Mismatches 2;	Indels 54;	Gaps 1;					
QY	1	GGAGGTTGAGTGAGCGAGATCATGCCAGCTGGGTGACAGTGAGACTCTGTCTCAAC	60						
Db	93	GGAGGTTGAACTGAGCAGAGATCATGCCAGCTGGGTGACAGTGAGACTCTGTCTCAAC	152						
QY	61	AGAATTAAAGAAAAAGAAAGAAAAAGAGAGAGAGAAATTCAGGCCAATTGTGG	120						
Db	153	AGAATTAAAGAAAAAGAAAGAAAAAGAGAGAGAGAAATTCAGGCCAATTGTGG	212						
QY	121	CATAGATTTTATCATATCTCTGGATTTTTCGATTTCTTTTCTCATCTGATTC	180						
Db	213	CATAGATTTTATCATATCTGGAATTTTTCGATTTCTTTTCTCATCTGATTC	272						
QY	181	GGAAGCCTGTGTGCCACCATCTCCAAAGGAGTTTACCTGCAGGGAATTTTAA	240						
Db	273	GGAAGCCTGTGTGTCCACCATCTCCAAAGGAGTTTACCTGCAGGGAATTTTAA	332						
QY	241	AGGCTGCTTCCCTGGGCAACAGGAGCCACCTGGGCGAGGAGCGCTTTTCAG	300						
Db	333	AGGCTGCTTCCCTGGGCAACAGGAGCCACCTGGGCGAG	371						
QY	301	GCCTTTTTCAGGAAGAGACGCTTTTTCAGGAAGAGAGAAAGTGCAGCTGA	360						
Db	372	-----GAGNAAGTGCAGCTGAAGAGGAAGTC	398						
QY	361	ACTTTACTAGGGGAGTCTCCATTTACTTTGGCACCATCATTTGGAGCAGGA	420						
Db	399	ACTTTACTAGGGGAGTCTCCATTTACTTTGGCACCATCATTTGGAGCAGGA	458						
QY	421	TCCTCTTAAGGCGCTGCTCAGAACACAGGCGAGGTGGGCATGTCTCTGAC	480						
Db	459	TCCTCTTAAGGCGCTGCTCAGAACACAGGCGAGGTGGGCATGTCTCTGAC	518						
QY	481	GTGTGTGGGCTCTGTCTACATTTTGGAGCTTTTGTCTATGCTCAATTTGG	540						
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QY	541	AAGAAATCTGGAGGTCAATACATATATTTTGGAAAGTCTTTGGTCCATTA	600						
Db	579	AAGAAATCTGGAGGTCAATACATATATTTTGGAAAGTCTTTGGTCCATTA	638						
QY	601	GTACGAGTCTGGGTGAACTCTCTATAAATACGCCCTGACGCTACTGCTGT	660						
Db	639	GTACGAGTCTGGGTGAACTCTCTATAAATACGCCCTGACGCTACTGCTGT	698						
QY	661	GCATTTTGGAGCGCTACATTTCTGGAGCAATTTTATTCAATGTGAATCC	720						
Db	699	GCATTTTGGAGCGCTACATTTCTGGAGCAATTTTATTCAATGTGAATCC	758						
QY	721	ATCAAGCTCATTAACGCTGTGGGCAATACTGTAGTCTATGCTCTTAATAG	780						





APPLICANT: Secrist, Heather  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
FILE REFERENCE: 210121.475C10  
CURRENT APPLICATION NUMBER: US/09/854,133  
CURRENT FILING DATE: 2001-05-11  
NUMBER OF SEQ ID NOS: 735  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 441  
LENGTH: 5981  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-854-133-441

Query Match 92.9%; Score 2080.8; DB 10; Length 5981;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 2146; Conservative 0; Mismatches 2; Indels 54; Gaps 1;  
QY 3 AGGTTGAAGTGACGAGATCATGCCAGCGTGGTGACAGTGAGACTCTGTCTCAAAACAG 62  
DB 1 AGGTTGAAGTGACGAGATCATGCCAGCGTGGTGACAGTGAGACTCTGTCTCAAAACAG 60  
QY 63 AATTAAGGAAAAAGAAAGAAAGAAAGAGAGAGAGAAATCCAGGCCAATTGTGGCA 122  
DB 61 AATTAAGGAAAAAGAAAGAAAGAAAGAGAGAGAGAAATCCAGGCCAATTGTGGCA 120  
QY 123 TAGATTTATCATATTCTGGATTTTGTGGATTTTGTGTTTCTCATCATCTGATTCAGG 182  
DB 121 TAGATTTATCATATTCTGGATTTTGTGGATTTTGTGTTTCTCATCATCTGATTCAGG 180  
QY 183 AAAGCTGTGTGTCACCATCTCCAAAGAGAGTTACCTGCGAGGAAATGTTAAACGGGAG 242  
DB 181 AAAGCTGTGTGTCACCATCTCCAAAGAGAGTTACCTGCGAGGAAATGTTAAACGGGAG 240  
QY 243 GCTGCTTCCCTGGGCAACAAGAGCCACTCGGAGGAGCGCTTTTCAGGAGAGAGCGC 302  
DB 241 GCTGCTTCCCTGGGCAACAAGAGCCACTCGGAGGAGCGCTTTTCAGGAGAGAGCGC 277  
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DB 278 -----GAGAAAGTGACGCTGAGAGAGAGTCA 306  
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DB 307 TTTACTGAGGGAGTCTCCATTATCATTTGGACACATATTGAGAGAGAGAGATCTCATCTC 366  
QY 423 TCCTAAGGCGTGTCCAGAACACGGGCGCTGGGCATGCTCTGACCATCTGGACGCT 482  
DB 367 TCCTAAGGCGTGTCCAGAACACGGGCGCTGGGCATGCTCTGACCATCTGGACGCT 426  
QY 483 GTGTGGGTCTGTCACTATTGAGCTTTGTCTTATGCTGAATTTGGAACTATATAA 542  
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QY 543 GAAATCTGAGGTCATTAACATATATTTGAGTCTTTGGTCCATACGAGCTTTGT 602  
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QY 963 ATATGCTGGCTGGTTTATACCTCAACTTTGTTACTGAGAGATGAGAAAACCTTGAAAAAAC 1022  
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DB 967 CATTCCTCTGCAATATGATATCATGCGCATTCATGCTGCTTTCAAAATGAGTGTGCTGACAAA 1026  
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QY 1143 GACCTTTTCTGAGCGGCTACTGGGAAATTTCTCAATAGCAGTTCCGATCTTTGTTGCCCT 1202  
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DB 1327 CGACAGCTCTTTGAAATTTCTCAGTTTTCAGAGTGGCTTTTATTTGAGGCTGGCAGTTGC 1386  
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DB 1507 GGACCCATTTAGTACAGGAGTTGGCTTCGTTCATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566  
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QY 1683 CAGAACATTAACAATAACTGGAAGTTGTACAGAGAGAGATGATGATGATGATGATGATGATGAT 1742  
DB 1627 CAGAACATTAACAATAACTGGAAGTTGTACAGAGAGAGATGATGATGATGATGATGATGATGAT 1686  
QY 1743 ACTTGAGATCTTGCAATCTGCCCAAGGGAGACACAAAATAGGATTTTACTTCAATTT 1802  
DB 1687 ACTTGAGATCTTGCAATCTGCCCAAGGGAGACACAAAATAGGATTTTACTTCAATTT 1746  
QY 1803 TCTGAAAGTCTAGAGAAATTAACAATTTGTTGATGATAAACAAGAGAGTCAAGTATTTTATTT 1862  
DB 1747 TCTGAAAGTCTAGAGAAATTAACAATTTGTTGATGATAAACAAGAGAGTCAAGTATTTTATTT 1806  
QY 1863 CATATATTTTAGCATATTCGAACTAATTTCTAGAGAAATTTAGTTATTAATCTCTAGTATGTT 1922  
DB 1807 CATATATTTTAGCATATTCGAACTAATTTCTAGAGAAATTTAGTTATTAATCTCTAGTATGTT 1866



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QY 1923 ATAGAAAGTGAATATATGACAGTTATCTTATGAGTGGCAAAATCTTGTAGTCTCTGATACCTA 1982
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RESULT 7
US-10-144-649A-441
; Sequence 441, Application US/10144649A
; Publication NO. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 441
; LENGTH: 5981
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-649A-441

Query Match 92.9%; Score 2080.8; DB 14; Length 5981;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 2146; Conservative 0; Mismatches 2; Indels 54; Gaps 1;

QY 3 AGGTTGAAGTGACGAGATCATGCCAGCTGGGTGACAGTGAGACTCTGTCTCAAAACAG 62
Db 1 AGGTTGAAGTGACGAGATCATGCCAGCTGGGTGACAGTGAGACTCTGTCTCAAAACAG 60
QY 63 AATTAAAGAAAAGAAAAGAAAAGAAAAGAGAGAGAGAAATTCAGGCCAATTTGGCA 122
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Qy AAAAGCATACATCATGATTTATGCAAGAGAGAGAGAGTA 2204  
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## RESULT 8

US-10-163-866-31  
; Sequence 31, Application US/10163866  
; Publication No. US20030027188A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: SLC7S AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-080C  
; CURRENT APPLICATION NUMBER: US/10/163,866  
; CURRENT FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/338,733  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/357,600  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31  
; LENGTH: 3144  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-163-866-31

## Query Match

Best Local Similarity 84.9%; Score 1900.2; DB 14; Length 3144;  
Matches 1966; Conservative 0; Mismatches 3; Indels 54; Gaps 1;  
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Qy 302 CTTTTCAGGAAGAGAGACGCCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCA 361  
Db 106 -----GAGAAAGTGCAGCTGAAGAGGAAAGTCA 133  
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Db 434 CATTTGGAGCTCATTTCTGGAACCATTTTATTCATGTGAATCCCTGAACTGGCA 493  
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QY 1142 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCGGATCTTTGTGTGCC 1201  
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QY 1274 TGTTCATCCAGCTTTGTTTTCCTTCAATGCTCTTCAATGTTGCCCTTTCCCTCTATT 1333  
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QY 1562 CGGACCAATTTAGTACAGGATTTGCTTTCGTCATCCTCTGAGTCCCTGGGATT 1621  
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QY 1334 CGGACCAATTTAGTACAGGATTTGCTTTCGTCATCCTCTGAGTCCCTGGGATT 1393  
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QY 1394 ATCTCTTTTATATATGGACAAAGAACCCAGTGGTTTATGAATATGTCAGAGAAATAA 1453  
Db |||||  
QY 1682 CCAGAACATTAACAATAATATCTGGAAGTTGTACAGAAAGAGATAGTATGAATAATG 1741  
Db |||||  
QY 1454 CCAGAACATTAACAATAATATCTGGAAGTTGTACAGAAAGAGATAGTATGAATAATG 1513  
Db |||||  
QY 1742 GACTTGAGATCTTGCCATCTGCCAAGGGAGACACAAAATAGGGATTTTACTCTATT 1801  
Db |||||  
QY 1514 GACTTGAGATCTTGCCAACTTGCCCAAGGGAGACACAAAATAGGGATTTTACTCTATT 1573  
Db |||||  
QY 1802 TTCTGAAAGCTAGAGAAATTAACAATTTGGTGATAAACAAGAGAGTCAGTTATTTTAT 1861  
Db |||||  
QY 1574 TTCTGAAAGCTAGAGAAATTAACAATTTGGTGATAAACAAGAGAGTCAGTTATTTTAT 1633  
Db |||||  
QY 1862 TCATATATTTTAGCATATTCGAATTAATTTCTAAGAAATTTAGTTATAACTCTATAGT 1921  
Db |||||  
QY 1634 TCATATATTTTAGCATATTCGAATTAATTTCTAAGAAATTTAGTTATAACTCTATAGT 1693  
Db |||||  
QY 1922 TATAGAAAGTGAATATGAGTTATTTCTATGAGTCGCAATTTCTTGAGTCTCTGATACCT 1981  
Db |||||  
QY 1694 TATAGAAAGTGAATATGAGTTATTTCTATGAGTCGCAATTTCTTGAGTCTCTGATACCT 1753  
Db |||||  
QY 1982 ACCTATTGGGGTTAGGAGAAAGACTAGACAAATTAATGTTGGTCATTCTCTCAACATA 2041  
Db |||||  
QY 1754 ACCTATTGGGGTTAGGAGAAAGACTAGACAAATTAATGTTGGTCATTCTCTCAACATA 1813  
Db |||||  
QY 2042 TGTTAGCAGCGCAAGAACCTTCAAAATGAAGACTGAGATTTTCTGATATATGGGTTT 2101  
Db |||||  
QY 1814 TGTTAGCAGCGCAAGAACCTTCAAAATGAAGACTGAGATTTTCTGATATATGGGTTT 1873  
Db |||||  
QY 2102 TGTAAAGATGTTTATACACATACAGATGCTCTATCTGTGAAAAGTGTTCATTTCTGA 2161  
Db |||||  
QY 1874 TGTAAAGATGTTTATACACATACAGATGCTCTATCTGTGAAAAGTGTTCATTTCTGA 1933  
Db |||||  
QY 2162 AAAAAAGCATACATCATGATTATGGCAAGAGGAGAGAGTA 2204  
Db |||||  
QY 1934 AAAAAAGCATACATCATGATTATGGCAAGAGGAGAGAGAA 1976  
Db |||||

## RESULT 9

US-10-163-866-29  
; Sequence 29, Application US/10163866  
; Publication No. US20030027189A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-080C  
; CURRENT APPLICATION NUMBER: US/10/163,866  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/338,733  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/357,600  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 29  
; LENGTH: 2482  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-163-866-29

Query Match 84.3%; Score 1888.2; DB 14; Length 2482;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 1965; Conservative 0; Mismatches 3; Indels 55; Gaps 2;  
QY 182 GAAAGCCTGTGTGTCCACCATCTCCAAAGAGGTTTACCTGCAGGAAATGTTTAAACGGGA 241  
Db |||||  
QY 239 GAAAGCCTGTGTGTCCACCATCTCCAAAGAGGTTTACCTGCAGGAAATGTTTAAACGGGA 298  
Db |||||  
QY 242 GGCTGCCTTCCCTGGGCAACAAAGAGCCACTCTGGGAGGAGCGCTTTTCAGGAAGAGACG 301  
Db |||||  
QY 299 GGCTGCCTTCCCTGGGCAACAAAGAGCCACTCTGGGAGGAGCGCTTTTCAGGAAGAGACG 336  
Db |||||  
QY 302 CTTTTTCAGGAAGAGACGCGCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCA 361  
Db |||||  
QY 362 CTTTACTGAGGGAGTCTCCATTATCATTTGGCCACCATCATTTGGAGCAGGATCTTCACTCT 421  
Db |||||  
QY 365 CTTTACTGAGGGAGTCTCCATTATCATTTGGCCACCATCATTTGGAGCAGGATCTTCACTCT 424  
Db |||||  
QY 422 CTCTAAGGGCGTGTCTCCAGAACACGGGCGAGCGTGGGCAATGCTCTGACCATCTGGAGCG 481  
Db |||||  
QY 425 CTCTAAGGGCGTGTCTCCAGAACACGGGCGAGCGTGGGCAATGCTCTGACCATCTGGAGCG 484  
Db |||||  
QY 482 TGTGTGGGGTCTGTCTCACTATTTTGGAGCTTTGTCTTATGCTGAATTTGGGAACAATATAA 541  
Db |||||  
QY 485 TATGTGGGGTCTGTCTCACTATTTTGGAGCTTTGTCTTATGCTGAATTTGGGAACAATATAA 544  
Db |||||  
QY 542 AGAATCTGAGGTCATTACACATATATTTGAGAGTCTTTGGTCCATTTCCAGGCTTTTG 601  
Db |||||  
QY 545 AGAATCTGAGGTCATTACACATATATTTTGGAAAGTCTTTGGTCCATTTACCAAGCTTTTG 604  
Db |||||  
QY 602 TACGAGTCTGGGTGGAACTCTCATATAATAGCCCTCGAGCTACTGCTGTGATATCCCTGG 661  
Db |||||  
QY 605 TACGAGTCTGGGTGGAACTCTCATATAATAGCCCTCGAGCTACTGCTGTGATATCCCTGG 664  
Db |||||  
QY 662 CATTTGGAGCTACATTTCTGGAACCAATTTTATTCAATGTGAAATCCCTGAACTTGGGA 721  
Db |||||  
QY 665 CATTTGGAGCTACATTTCTGGAACCAATTTTATTCAATGTGAAATCCCTGAACTTGGGA 724  
Db |||||  
QY 722 TCAAGCTCATTAAGCTGTGGGCAATTAATGTAGTATGCTCTTAAATAGCATGAGTGTCA 781  
Db |||||  
QY 725 TCAAGCTCATTAAGCTGTGGGCAATTAATGTAGTATGCTCTTAAATAGCATGAGTGTCA 784  
Db |||||

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QY 782 GCTGAGGCGCCGGATCCAGATTTCTTAACCTTTTGCAGGCTCAGCAATTTCTGATAA 841
Db 785 GCTGAGGCGCCGGATCCAGATTTCTTAACCTTTTGCAGGCTCAGCAATTTCTGATAA 844
QY 842 TTATAGTCCCTGGAGTTATGCGAGCTAAATTAAGGTCAAACGCGAGCAATTTAAAGCGCCT 901
Db 845 TTATAGTCCCTGGAGTTATGCGAGCTAAATTAAGGTCAAACGCGAGCAATTTAAAGCGCCT 904
QY 902 TTTCAGGAAGAGATTCAGATTAATGCGGTTGCCACTGCTTTTATATGGAATGTATG 961
Db 905 TTTCAGGAAGAGATTCAGATTAATGCGGTTGCCACTGCTTTTATATGGAATGTATG 964
QY 962 CATATGCTGGCTGGTTTACCTCAACTTTGTACTGAAGAGTAGAAGACCCCTGAAAAA 1021
Db 965 CATATGCTGGCTGGTTTACCTCAACTTTGTACTGAAGAGTAGAAGACCCCTGAAAAA 1024
QY 1022 CAATTCCCTTTCAGATATGATATCATGCGCAATTTGTACCAATTTGGCTATGTGCAAA 1081
Db 1025 CCATTTCCCTTTCAGATATGATATCATGCGCAATTTGTACCAATTTGGCTATGTGCAAA 1084
QY 1082 ATGTGSCCTACTTTACGACCAATTAATGCTGAGAGCTGCTGCTTTCAATGCAAGTGGCAG 1141
Db 1085 ATGTGSCCTACTTTACGACCAATTAATGCTGAGAGCTGCTGCTTTCAATGCAAGTGGCAG 1144
QY 1142 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCAATAGCAGTTCCGATCTTTGTGCC 1201
Db 1145 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCAATAGCAGTTCCGATCTTTGTGCC 1204
QY 1202 TCTCTGCTTTGGCTCCATGAACGGTGGTGTGTTGCTGTCTCCAGGTTATTTCTATGTTG 1261
Db 1205 TCTCTGCTTTGGCTCCATGAACGGTGGTGTGTTGCTGTCTCCAGGTTATTTCTATGTTG 1264
QY 1262 CGTCTCGAGAGGCTCACCTTCAGAGAAATCTCTCCATGATTCATCTCCGACGACATC 1321
Db 1265 CGTCTCGAGAGGCTCACCTTCAGAGAAATCTCTCCATGATTCATCTCCGACGACATC 1324
QY 1322 CTCTACAGCTGTATTGTTTTCACCCCTTTGACAAATGATATGCTCTTCTCGAGACC 1381
Db 1325 CTCTACAGCTGTATTGTTTTCACCCCTTTGACAAATGATATGCTCTTCTCGAGACC 1384
QY 1382 TCGACAGTCTTTTGAATTTCTCAGTTTTCAGGTGGCTTTTATTTGGGCTGGCAGTTG 1441
Db 1385 TCGACAGTCTTTTGAATTTCTCAGTTTTCAGGTGGCTTTTATTTGGGCTGGCAGTTG 1444
QY 1442 CTGGCTGATTTATCTTCGATACAAATGCCAGATATGATCGTCTCTTCAAGTGCCAC 1501
Db 1445 CTGGCTGATTTATCTTCGATACAAATGCCAGATATGATCGTCTCTTCAAGTGCCAC 1504
QY 1502 TGTTCAATCCAGCTTTGTTTTCCTTCATATGCTCTTTCATGTTGCCCTTTCCCTCTATT 1561
Db 1505 TGTTCAATCCAGCTTTGTTTTCCTTCATATGCTCTTTCATGTTGCCCTTTCCCTCTATT 1564
QY 1562 CGGACCCATTTAGTACAGGATTTGGCTTGGTCATCACTGATCTGAGTCCGTGGGTATT 1621
Db 1565 CGGACCCATTTAGTACAGGATTTGGCTTGGTCATCACTGATCTGAGTCCGTGGGTATT 1624
QY 1622 ATCTCTTTATATATGGACAGAAACCCAGGTGTTTGTAGATAATGTCAGAGAAATAA 1681
Db 1625 ATCTCTTTATATATGGACAGAAACCCAGGTGTTTGTAGATAATGTCAGAGAAATAA 1684
QY 1682 CCAGAACATTAATAATCTGGAAGTTGTACAGAGAGAGATAAGTTATGAACATAATG 1741
Db 1685 CCAGAACATTAATAATCTGGAAGTTGTACAGAGAGAGATAAGTTATGAACATAATG 1744
QY 1742 GACTTGAGATCTTGGCAATCTGCCAAGGGAGACACAAAATAGGGATTTTACTTCATT 1801
Db 1745 GACTTGAGATCTTGGCAATCTGCCAAGGGAGACACAAAATAGGGATTTTACTTCATT 1804
QY 1802 TTCTGAAAGTCTAGAGAAATTAACAATTTGGTGATAAACAAAGGAGTCAGTTATTTTAT 1861
Db 1805 TTCTGAAAGTCTAGAGAAATTAACAATTTGGTGATAAACAAAGGAGTCAGTTATTTTAT 1864
QY 1862 TCATATATTTAGCATATTTCCAACTAATTTCTTAAGAAATTTAGTTATTAACCTATGTAGT 1921
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Db 1865 TCATATATTTAGCATATTTCCAACTAATTTCTTAAGAAATTTAGTTATTAACCTATGTAGT 1924
QY 1922 TATAGAAAGTCAATATGCAAGTTATTTCTATGAGTCGCAAAATTTCTGAGTCTCTGATAGCT 1981
Db 1925 TATAGAAAGTCAATATGCAAGTTATTTCTATGAGTCGCAAAATTTCTGAGTCTCTGATAGCT 1984
QY 1982 ACCTATTGGGTTAGGAGAAAAGCTAGCAAAATTAATGTTGGTCATTCTCTCAACAATA 2041
Db 1985 ACCTATTGGGTTAGGAGAAAAGCTAGCAAAATTAATGTTGGTCATTCTCTCAACAATA 2044
QY 2042 TGTTAGCAGCGCAAGAACCCTTCAAAATTTGAAGACTGAGATTTTCTGTATATATGGGTTT 2101
Db 2045 TGTTAGCAGCGCAAGAACCCTTCAAAATTTGAAGACTGAGATTTTCTGTATATATGGGTTT 2104
QY 2102 TGTAAAGATGGTTTACACACTACAGATGCTATCTATCTGTGAAAAGTGTTCATTTCTGA 2161
Db 2105 TGT-AAAGATGGTTTACACACTACAGATGCTATCTATCTGTGAAAAGTGTTCATTTCTGA 2163
QY 2162 AAAAAGCATACATCATGATTTATGCGAAAGAGGAGAGAGGTA 2204
Db 2164 AAAAAGCATACATCATGATTTATGCGAAAGAGGAGAGAGAA 2206

RESULT 10
US-10-133-013-40
; Sequence 40, Application US/10133013
; Publication No. US20030166903A1
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 2041
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 406992.1
; NAME/KEY: unsure
; LOCATION: 1923, 1998, 2026
; OTHER INFORMATION: a, t, c, g, or other
US-10-133-013-40

Query Match 76.6%; Score 1715; DB 12; Length 2041;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 1790; Conservative 0; Mismatches 3; Indels 55; Gaps 2;

QY 182 GAAAGCCTGTTGTGTCCACCATCTCCAAAGAGAGTTACCTGCGAGGAAATGTT-AAACGG 240
Db 248 GAAAGCCTGTTGTGTCCACCATCTCCAAAGAGAGTTACCTGCGAGGAAATGTTAAACGG 307
QY 241 AGGCTGCTTCCCTGGGCAACAGGAGCCACCTGGGCGAGGACGCCCTTTTCAGGAGAGAC 300
Db 308 AGGCTGCTTCCCTGGGCAACAGGAGCCACCTGGGCGAGGAGC----- 346
QY 301 GCCTTTTCAGGAAGAGACGCTTTTCAGGAAGAGAGAAAGTCAGCTGAAGAGAAAGTC 360
Db 347 -----GAGAAAGTCAGCTGAAGAGAAAGTC 373
QY 361 ACTTTACTGAGGGAGTCTCCATTATCATTGGCAACCATTATGGAGCAGGAATCTTCATC 420
Db 374 ACTTTACTGAGGGAGTCTCCATTATCATTGGCACCATTATGGAGCAGGAATCTTCATC 433
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QY 421 TCTCTAAGGGGCTGCTCAGAAACGGGACGGTGGGCGATGTCTCTGACCACTGGACG 480  
Db 434 TCTCTAAGGGGCTGCTCAGAAACGGGACGGTGGGCGATGTCTCTGACCACTGGACG 493  
QY 481 GTGTGTGGGCTCTGCTCACTATTTGGAGCTTTGCTTATGCTGAATTTGGGAACAACATA 540  
Db 494 GTGTGTGGGCTCTGCTCACTATTTGGAGCTTTGCTTATGCTGAATTTGGGAACAACATA 553  
QY 541 AAGAAATCTGGAGGTCATTACACATATATTTTGGAAAGTCTTTGGTCCCATTAACCACTTTT 600  
Db 554 AAGAAATCTGGAGGTCATTACACATATATTTTGGAAAGTCTTTGGTCCCATTAACCACTTTT 613  
QY 601 GTACAGTCTGGTGGAACTCTCTATAATAGCCCTCGAGCTACGTCTGTGATATCCCTG 660  
Db 614 GTACAGTCTGGTGGAACTCTCTATAATAGCCCTCGAGCTACGTCTGTGATATCCCTG 673  
QY 661 GCATTTGACGCTACATTTCTGGAACCAATTTTATTTCAATGTGAATCCCTGAACTTGG 720  
Db 674 GCATTTGACGCTACATTTCTGGAACCAATTTTATTTCAATGTGAATCCCTGAACTTGG 733  
QY 721 ATCAAGCTCATTTACAGCTGTGGCATAACTGTAGTATGATGGTCTTAATAATAGCATGATGTC 780  
Db 734 ATCAAGCTCATTTACAGCTGTGGCATAACTGTAGTATGATGGTCTTAATAATAGCATGATGTC 793  
QY 781 AGCTGGAGCGCCGGATCCAGATTTCTTAACCTTTTGCATGCTCACAGCAATTTCTGATA 840  
Db 794 AGCTGGAGCGCCGGATCCAGATTTCTTAACCTTTTGCATGCTCACAGCAATTTCTGATA 853  
QY 841 ATTATAGTCCCTGGATTTATCAGCTAATTAAGTCAAAACGACAACTTTAAAGACGCC 900  
Db 854 ATTATAGTCCCTGGATTTATCAGCTAATTAAGTCAAAACGACAACTTTAAAGACGCC 913  
QY 901 TTTTCAGGAAGAGATTCAAGTATTACGGGTGTCACCTGGCTTTTATTTATGGAATGTAT 960  
Db 914 TTTTCAGGAAGAGATTCAAGTATTACGGGTGTCACCTGGCTTTTATTTATGGAATGTAT 973  
QY 961 GCATATGCTGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAACCCCTGAAAAA 1020  
Db 974 GCATATGCTGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAACCCCTGAAAAA 1033  
QY 1021 ACCATTCCTCTGCAATATGATATCATGCGCATTTGTCCACCATTTGGTATGCTGACACA 1080  
Db 1034 ACCATTCCTCTGCAATATGATATCATGCGCATTTGTCCACCATTTGGTATGCTGACACA 1093  
QY 1081 AATGTGCTCTACTTTACGACCAATTAATGCTGAGGAGTGTGCTTTTCAAAATGCAAGTGCCA 1140  
Db 1094 AATGTGCTCTACTTTACGACCAATTAATGCTGAGGAGTGTGCTTTTCAAAATGCAAGTGCCA 1153  
QY 1141 GTGACCTTTTCTGAGCGGCTACTCGGAAAATTTCTCATATAGCAGTTCGATTTTGTGCC 1200  
Db 1154 GTGACCTTTTCTGAGCGGCTACTCGGAAAATTTCTCATATAGCAGTTCGATTTTGTGCC 1213  
QY 1201 CTCTCTGCTTTGCTCCATGAACGGTGGTGTGTTTTGTTTTGCTCTCCAGGTTATTTATGTT 1260  
Db 1214 CTCTCTGCTTTGCTCCATGAACGGTGGTGTGTTTTGTTTTGCTCTCCAGGTTATTTATGTT 1273  
QY 1261 GCGTCTCGAGAGGCTACCTTTCCAGAAATCTCTCCATGATTTATGTCGCGCAACACACT 1320  
Db 1274 GCGTCTCGAGAGGCTACCTTTCCAGAAATCTCTCCATGATTTATGTCGCGCAACACACT 1333  
QY 1321 CCTCTACAGCTGTATTTGTTGACCCCTTTGACAAATGATATGCTCTCTCTGGAGAC 1380  
Db 1334 CCTCTACAGCTGTATTTGTTGACCCCTTTGACAAATGATATGCTCTCTCTGGAGAC 1393  
QY 1381 CTGACAGCTTTTGAATTTTCCAGTTTGGCAGTGGCTTTTATTTGGGCTGGCAGTT 1440  
Db 1394 CTGACAGCTTTTGAATTTTCCAGTTTGGCAGTGGCTTTTATTTGGGCTGGCAGTT 1453  
QY 1441 GCTGGGCTGATTTATCTTCGATACAAATGCGCATATGATGCTCTCTTTCAAGGTGCCA 1500  
Db 1454 GCTGGGCTGATTTATCTTCGATACAAATGCGCATATGATGCTCTCTTTCAAGGTGCCA 1513  
QY 1501 CTGTTTCAATCCAGCTTTGTTTTCTTCAATGCTCTTCTATGTTGCTCTTCCCTCTAT 1560

Db 1514 CTGTTTCATCCAGCTTTGTTTTCTTTCATGCTCTTTCATGTTGCCCTTCCCTCTAT 1573  
QY 1561 TCGAGCCCATTTAGTACAGGATTTGGCTTGTCTATCATCTGACTGGAGTCCCTGCGTAT 1620  
Db 1574 TCGAGCCCATTTAGTACAGGATTTGGCTTGTCTATCATCTGACTGGAGTCCCTGCGTAT 1633  
QY 1621 TATCTCTTTTATATATGCGGACAGAAACCCAGGTGGTTTGAATAATGTCTAGAAAAATA 1680  
Db 1634 TATCTCTTTTATATGCGGACAGAAACCCAGGTGGTTTGAATAATGTCTAGAAAAATA 1693  
QY 1681 ACCAGAACATTTACAAATAATACTGGAAAGTTGTATCCAGAAAGATAAGTTATGAACATAAT 1740  
Db 1694 ACCAGAACATTTACAAATAATACTGGAAAGTTGTATCCAGAAAGATAAGTTATGAACATAAT 1753  
QY 1741 GGACTTGAGATCTTTGGCAATCTGCCCAAGGGGAGACACAAAATAGGATTTTACTTTCAT 1800  
Db 1754 GGACTTGAGATCTTTGGCAATCTGCCCAAGGGGAGACACAAAATAGGATTTTACTTTCAT 1813  
QY 1801 TTTCTGAAAGTCTAGAGAAATTAACAATTTTGGTGATAAACAAAAGGAGTCAAGTTATTTTA 1860  
Db 1814 TTTCTGAAAGTCTAGAGAAATTAACAATTTTGGTGATAAACAAAAGGAGTCAAGTTATTTTA 1873  
QY 1861 TTCAATATTTTATGCAATTTTGAACATAATTTCTAAGAAATTTTATGTTATAAATCTTATCTAG 1920  
Db 1874 TTCAATATTTTATGCAATTTTGAACATAATTTCTAAGAAATTTTATGTTATAAATCTTATCTAG 1933  
QY 1921 TTATAGAAAGTGAATATGCAATTTTCTATGAGTCGCAAAATTTCTGAGTCTCTGATACC 1960  
Db 1934 TTATAGAAAGTGAATATGCAATTTTCTATGAGTCGCAAAATTTCTGAGTCTCTGATACC 1993  
QY 1981 TACTATTTGGGTTTAGGAGAAAAGACTAGACAAATTTACTATGTGTCTAT 2028  
Db 1994 TACNATTTGGGTTTAGGAGAAAAGACTAGACAAATTTACTATGTGTCTAT 2041

## RESULT 11

US-10-247-671-78  
; Sequence 78, Application US/10247671  
; Publication No. US20030194721A1  
; GENERAL INFORMATION:  
; APPLICANT: Mikita, Thomas  
; APPLICANT: Shiffman, Dov  
; APPLICANT: Porter, Gordon, J.  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS  
; FILE REFERENCE: PA-0050 US  
; CURRENT APPLICATION NUMBER: US/10/247,671  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/323,784  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: PERL Program  
; SEQ ID NO 78  
; LENGTH: 2041  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20030194721A1 406992.1  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 1923, 1998, 2026  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-247-671-78

Query Match 76.6%; Score 1715; DB 12; Length 2041;  
Best Local Similarity 96.9%; Pred. No. 0;  
Matches 1790; Conservative 0; Mismatches 3; Indels 55; Gaps 2;  
QY 182 GAAAGCCTGTGTGTCCACCATCTCCAAAGGAGTTTACCTGACGGGAAATGTT-AAACGGG 240  
Db 248 GAAAGCCTGTGTGTCCACCATCTCCAAAGGAGTTTACCTGACGGGAAATGTTAAACGGG 307

QY	241	AGGCTGCTTCCCTGGGCAACAAGGAGCCACCTGGGCGAGCACGCTTTTCAGGAAGAC	300
Db	308	AGGCTGCTTCCCTGGGCAACAAGGAGCCACCTGGGCGAG	346
QY	301	GCCTTTTCGGAAGAGACGCGCTTTTCAGGAAGAGAAAGTGCAGCTGAAGAGGAAGTC	360
Db	347	-----GAGAAAGTGCAGCTGAAGAGGAAGTC	373
QY	361	ACTTTACTAGGGGAGTCTCCATTATCATTGGCACCATCATTTGGAGCAGGAATCTTCATC	420
Db	374	ACTTTACTAGGGGAGTCTCCATTATCATTGGCACCATCATTTGGAGCAGGAATCTTCATC	433
QY	421	TCTCCTAAGGGCGTCTCCAGAACACGGGACAGCGTGGGCATGTCTCTGCACCATCTGGACG	480
Db	434	TCTCCTAAGGGCGTCTCCAGAACACGGGACAGCGTGGGCATGTCTCTGCACCATCTGGACG	493
QY	481	GTGTGTGGGTCTGTGCATTTATTTGGAGCTTTGTCTTATGCTGAATTTGGGAAACAACATATA	540
Db	494	GTGTGTGGGTCTGTGCATTTATTTGGAGCTTTGTCTTATGCTGAATTTGGGAAACAACATATA	553
QY	541	AAGAAATCTGGAGGTCAATTACACATATATTTTGGAAAGTCTTTGGTCCATTACCAGCTTTT	600
Db	554	AAGAAATCTGGAGGTCAATTACACATATATTTTGGAAAGTCTTTGGTCCATTACCAGCTTTT	613
QY	601	GTACGAGTCTGGGTGGAACTCCTCATTAATACGCCCTGCAGCTACTGCTGTGATATCCCTG	660
Db	614	GTACGAGTCTGGGTGGAACTCCTCATTAATACGCCCTGCAGCTACTGCTGTGATATCCCTG	673
QY	661	GCAATTTGGAGCGCTACATTTCTGGAAACCAATTTTATTCAATGTGAATFCCCTGAACTTGG	720
Db	674	GCAATTTGGAGCGTACATTTCTGGAAACCAATTTTATTCAATGTGAATFCCCTGAACTTGG	733
QY	721	ATCAAGTCAATTACAGCTGTGGGCATAACTGTGTAGTAGTGTCTTAATACATGAGTGTCT	780
Db	734	ATCAAGTCAATTACAGCTGTGGGCATAACTGTGTAGTAGTGTCTTAATACATGAGTGTCT	793
QY	781	AGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTTCGAAGCTCAGCAATCTCTGATA	840
Db	794	AGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTTCGAAGCTCAGCAATCTCTGATA	853
QY	841	ATTATAGTCCCTGGAGTTATGCACTAATTTAAAGGTCAAAACGCAAGACTTTTAAAGACGCC	900
Db	854	ATTATAGTCCCTGGAGTTATGCACTAATTTAAAGGTCAAAACGCAAGACTTTTAAAGACGCC	913
QY	901	TTTTTCAGGAAGAGATCAAGTATTACGGGTTGCCACTGGCTTTTATTATGGAATGTAT	960
Db	914	TTTTTCAGGAAGAGATCAAGTATTACGGGTTGCCACTGGCTTTTATTATGGAATGTAT	973
QY	961	GCATATGCTGGCTGGTTTTACCTCAACTTTGTACTGAAGAAGTAGAAAAACCTCGAAAAA	1020
Db	974	GCATATGCTGGCTGGTTTTACCTCAACTTTGTACTGAAGAAGTAGAAAAACCTCGAAAAA	1033
QY	1021	ACCATTTCCCTTGGCAATATGTATATCATGGCCATTTGTCAACATTTGGCTATGTCTGACA	1080
Db	1034	ACCATTTCCCTTGGCAATATGTATATCATGGCCATTTGTCAACATTTGGCTATGTCTGACA	1093
QY	1081	AATGTGGCTTACTTTACGACCAATTAATGCTGAGGAGCTGCTGCTTTCAAAATGAGTGGCA	1140
Db	1094	AATGTGGCTTACTTTACGACCAATTAATGCTGAGGAGCTGCTGCTTTCAAAATGAGTGGCA	1153
QY	1141	GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCGATCTTTGTGGCC	1200
Db	1154	GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCGATCTTTGTGGCC	1213
QY	1201	CTCTCTGCTTTTGGCTCCATGAACGGTGGTGTGTGCTGTCTCCAGTTATTCTATGTT	1260
Db	1214	CTCTCTGCTTTTGGCTCCATGAACGGTGGTGTGTGCTGTCTCCAGTTATTCTATGTT	1273
QY	1261	GGCTCTCGAGGGTCACTTCCAGAAATCCTCTCCATGATTCATGTCCGACAGCACACT	1320
Db	1274	GGCTCTCGAGGGTCACTTCCAGAAATCCTCTCCATGATTCATGTCCGACAGCACACT	1333

Qy	1321	CCTCTACCAAGCTGTATGTGTTTTGGACCCCTTTGACAAATGAATAGCTCTTCTCTGGAGAC	1381
Db	1334	CCTCTACCAAGCTGTATGTGTTTTGGCACCCCTTTGACAAATGATAATAGTCTTCTCTGGAGAC	1393
Qy	1381	CTGCAGAGCTCTTTTGAATTTCCCTCAGTTTTGCCCAGGTGGCTTTTATATGGCGCTGGCAGTT	1440
Db	1394	CTGCAGAGCTCTTTTGAATTTCCCTCAGTTTTGCCCAGGTGGCTTTTATATGGCGCTGGCAGTT	1453
Qy	1441	GCTGGGCTGATTTATCTTTGGATACAAATGCCAGATATGCATCGTCTTTTCAAGGTGCCA	1500
Db	1454	GCTGGGCTGATTTATCTTTGGATACAAATGCCAGATATGCATCGTCTTTTCAAGGTGCCA	1513
Qy	1501	CTGTTCAATCCCAAGCTTTGTTTTCCCTTCACATGCTCTTCATAGTGGCTGCCCTTCCCTCTAT	1560
Db	1514	CTGTTCAATCCCAAGCTTTGTTTTCCCTTCACATGCTCTTCATAGTGGCTGCCCTTCCCTCTAT	1573
Qy	1561	TCGGACCCATTTTAGTACAGGGAATGGCTTCGTCTCATCACTCTGACTGGAGTCCCTGGGTAT	1620
Db	1574	TCGGACCCATTTTAGTACAGGGAATGGCTTCGTCTCATCACTCTGACTGGAGTCCCTGGGTAT	1633
Qy	1621	TATCTCTTTTATTATATGGGACAGAAACCCAGGTGGTTTAGAATAATATCTCAGAGAAAAATA	1680
Db	1634	TATCTCTTTTATTATATGGGACAGAAACCCAGGTGGTTTAGAATAATATCTCAGAGAAAAATA	1693
Qy	1681	ACCAGAACATTACAAATAATPACTTGGAAAGTTGTACCAGAGAAAGATAAGTTATCAACTAAT	1740
Db	1694	ACCAGAACATTACAAATAATPACTTGGAAAGTTGTACCAGAGAGAGATAAGTTATCAACTAAT	1753
Qy	1741	GGACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAAATAGGGAATTTTTACTTTTCAT	1800
Db	1754	GGACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAAATAGGGAATTTTTACTTTTCAT	1813
Qy	1801	TTTCTGAAAGCTTAGAGAAATTACAACTTTTGGTGATATAACAAAAGGAGTCAAGTTATTTTTA	1860
Db	1814	TTTCTGAAAGCTTAGAGAAATTACAACTTTTGGTGATATAACAAAAGGAGTCAAGTTATTTTTA	1873
Qy	1861	TTCATATATTTTAGCATATTCGAACTAAATTTCTTAAGAAATTTAGTTATTAACCTATGTAG	1920
Db	1874	TTCATATATTTTAGCATATTCGAACTAAATTTCTTAAGAAATTTAGTTATTAACCTATGTAG	1933
Qy	1921	TTATAGAAAGTGAATATGCAGTTTATCTATGAGTCGCACAAATTTCTTGAGTCTCTGATACC	1980
Db	1934	TTATAGAAAGTGAATATGCAGTTTATCTATGAGTCGCACAAATTTCTTGAGTCTCTGATACC	1993
Qy	1981	TACTATTTGGGGTTAGAGAAAAAGATAGACAAATTAATCTATGTGGTCAAT	2028
Db	1994	TACNATTTGGGGTTAGAGAAAAAGATAGACAAATTAATCTATGTGGTCAAT	2041

RESULT 12  
US-10-163-866-30  
; Sequence 30, Application US/10153866  
; Publication No. US20030027188A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-080C  
; CURRENT APPLICATION NUMBER: US/10/163,866  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/338,733  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/357,600  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30  
; LENGTH: 1861

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-163-866-30

Query Match      68.8%; Score 1540.8; DB 14; Length 1861;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 1606; Conservative 0; Mismatches 2; Indels 54; Gaps 1;

QY 182 GAAAGCCTGTGTGTCACCATCTCCAAAGAGGAGTTTACCTGCAGGGAATGTTAAAGCGGA 241
Db      |||
QY 243 GAAAGCCTGTGTGTCACCATCTCCAAAGAGGAGTTTACCTGCAGGGAATGTTAAAGCGGA 302
Db      |||
QY 242 GCGTGCCTTCCCTGGGCAACAAGAGCCACCTGGGAGAGCGCCTTTTCAGGAAGAGAGCG 301
Db      |||
QY 303 GCGTGCCTTCCCTGGGCAACAAGAGCCACCTGGGAG----- 340
Db      |||
QY 302 CCTTTTCAGGAAGAGAGCGCTTTTCAGGAAGAGAGAGAGTGCAGCTGAAGAGGAAGTCA 361
Db      |||
QY 341 -----GAGAAAGTGCAGCTGAAGAGGAAGTCA 368
Db      |||
QY 362 CTTTACTGAGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATCT 421
Db      |||
QY 369 CTTTACTGAGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATCT 428
Db      |||
QY 422 CTCCTAAGGCGTGTCTCAGAAACAAGGAGCGGTGGGCAATGCTCTGACCATCTGGAAGG 481
Db      |||
QY 429 CTCCTAAGGCGTGTCTCAGAAACAAGGAGCGGTGGGCAATGCTCTGACCATCTGGAAGG 488
Db      |||
QY 482 TGTGTGGGCTCTCTGCATATTTGGAGCTTCTCTATCTCTGAATTTGGAAACAACATATAA 541
Db      |||
QY 489 TGTGTGGGCTCTCTGCATATTTGGAGCTTGTCTTATGCTGAAATTTGGGAAACAACATATAA 548
Db      |||
QY 542 AGAAATCTGAGGTCATTACACATATATTTTGGAAAGTCTTTGGTCCATTACCAGCTTTTG 601
Db      |||
QY 549 AGAAATCTGAGGTCATTACACATATATTTTGGAGTCTTTGGTCCATTACCAGCTTTTG 608
Db      |||
QY 602 TACGAGTCTGGTGGAACTCTCTCAATAAATACGCGCTGCACTACTGCTGATATCCCTGG 661
Db      |||
QY 609 TACGAGTCTGGTGGAACTCTCTCAATAAATACGCGCTGCACTACTGCTGATATCCCTGG 668
Db      |||
QY 662 CATTTGGAGCGTACATCTCGGAACCAATTTTATTCATGTGAATCCCTGAACTTGGGA 721
Db      |||
QY 669 CATTTGGAGCGTACATCTCGGAACCAATTTTATTCATGTGAATCCCTGAACTTGGGA 728
Db      |||
QY 722 TCAAGCTCATTAACAGTGTGGGCAATACTGTAGTGTCTTAATAGCATGAGTGTCA 781
Db      |||
QY 729 TCAAGCTCATTAACAGTGTGGGCAATACTGTAGTGTCTTAATAGCATGAGTGTCA 788
Db      |||
QY 782 GCTGAGGCGCGGATCCAGATTTTCTTAAACCTTTTGAAGCTCACAGCAATTTCTGATAA 841
Db      |||
QY 789 GCTGAGGCGCGGATCCAGATTTTCTTAAACCTTTTGAAGCTCACAGCAATTTCTGATAA 848
Db      |||
QY 842 TTATAGTCCCTGGAGTTATGAGCTAATTAAGGTCAAACGAGCAACTTTAAAGCGCT 901
Db      |||
QY 849 TTATAGTCCCTGGAGTTATGAGCTAATTAAGGTCAAACGAGCAACTTTAAAGCGCT 908
Db      |||
QY 902 TTTCAAGAGAGATTCAGATTAACGCGTTGCCACTGCTTTTATTTATGGAATGATG 961
Db      |||
QY 909 TTTCAAGAGAGATTCAGATTAACGCGTTGCCACTGCTTTTATTTATGGAATGATG 968
Db      |||
QY 962 CATATGCTGGCTGTTTACCTCAACCTTTGTTATCTGAAGAGTGAAGAACCTGAAAAA 1021
Db      |||
QY 969 CATATGCTGGCTGTTTACCTCAACCTTTGTTATCTGAAGAGTGAAGAACCTGAAAAA 1028
Db      |||
QY 1022 CCATTCCCTCTGCATATGATATCCATGGCCATTGTACCATTTGGCTATGTGCTGACAA 1081
Db      |||
QY 1029 CCATTCCCTCTGCATATGATATCCATGGCCATTGTACCATTTGGCTATGTGCTGACAA 1088
Db      |||
QY 1082 ATGTGCGCTACTTTACGACCAATTAATGCTGAGGAGCTGCTGCTTTTCAAAATGAGTGGCAG 1141
Db      |||
QY 1089 ATGTGCGCTACTTTACGACCAATTAATGCTGAGGAGCTGCTGCTTTTCAAAATGAGTGGCAG 1148
Db      |||
QY 1142 TGACCTTTTCTGAGGGGCTACTGGGAAATTTTCTATTAGCAGTTCGGATCTTTTGTGCCC 1201
Db      |||
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Db      |||
QY 1149 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCGATCTTTGTGCCCC 1208
Db      |||
QY 1202 TCTCTGCTTTGGCTCCATGAACGGTGTGTGTTTGTCTGTCTCCAGGTTTATCTATGTTG 1261
Db      |||
QY 1209 TCTCTGCTTTGGCTCCATGAACGGTGTGTGTTTGTCTGTCTCCAGGTTTATCTATGTTG 1268
Db      |||
QY 1262 GGTCTCGAGAGGGTCACTTCCAGAAATCTCTCCATGATTCATGTCGCAAGCACTC 1321
Db      |||
QY 1269 GGTCTCGAGAGGGTCACTTCCAGAAATCTCTCCATGATTCATGTCGCAAGCACTC 1328
Db      |||
QY 1322 CTCTACCAAGCTGTATGTTTGTGACCCCTTTCACAAATGATATGCTCTCTCTCGAGAC 1381
Db      |||
QY 1329 CTCTACCAAGCTGTATGTTTGTGACCCCTTTCACAAATGATATGCTCTCTCTCGAGAC 1388
Db      |||
QY 1382 TCGACAGCTTTTGAATTTCTCAGTTTTCAGTTTTCAGAGTGGCTTTTATTTGGGCTGGCAGTTG 1441
Db      |||
QY 1389 TCGACAGCTTTTGAATTTCTCAGTTTTCAGTTTTCAGAGTGGCTTTTATTTGGGCTGGCAGTTG 1448
Db      |||
QY 1442 CTGGGCTCATTTATCTTCGATACAAATGCCAGATATGATCGTCTCTTCAAGGTGCCAC 1501
Db      |||
QY 1449 CTGGGCTCATTTATCTTCGATACAAATGCCAGATATGATCGTCTCTTCAAGGTGCCAC 1508
Db      |||
QY 1502 TGTTCATCCAGCTTTGTTTTCCTTTCACATGCTCTTTCATGTTTGCCTTTTCCCTCTATT 1561
Db      |||
QY 1509 TGTTCATCCAGCTTTGTTTTCCTTTCACATGCTCTTTCATGTTTGCCTTTTCCCTCTATT 1568
Db      |||
QY 1562 CGGACCCATTTAGTACAGGGATTTGGTTCGTCATCATCTGACGTGAGTCCCTGCGTATT 1621
Db      |||
QY 1569 CGGACCCATTTAGTACAGGGATTTGGTTCGTCATCATCTGACGTGAGTCCCTGCGTATT 1628
Db      |||
QY 1622 ATCTCTTATTTATATGGGACAAAGAACCCAGTGGTGTAGATATGTCAGAGAAATAA 1681
Db      |||
QY 1629 ATCTCTTATTTATATGGGACAAAGAACCCAGTGGTGTAGATATGTCAGAGAAATAA 1688
Db      |||
QY 1682 CCAGAACATTTACAATTAATCTGGAAGTTGTACAGAGAAAGATTAAGTTGAACATAATG 1741
Db      |||
QY 1689 CCAGAACATTTACAATTAATCTGGAAGTTGTACAGAGAAAGATTAAGTTGAACATAATG 1748
Db      |||
QY 1742 GACTTGAGATCTTGGCAATCTGCCAAGGGGAGAGACAAAAATAGGATTTTACTTCATT 1801
Db      |||
QY 1749 GACTTGAGATCTTGGCAATCTGCCAAGGGGAGAGACAAAAATAGGATTTTACTTCATT 1808
Db      |||
QY 1802 TTCTGAAAGCTACAGAAATTAACACTTTTGTGATTAACAAAA 1843
Db      |||
QY 1809 TTCTGAAAGCTACAGAAATTAACACTTTTGTGATTAACAAAA 1850
Db      |||

RESULT 13
US-10-163-866-33
; Sequence 33, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLIC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 1542
; TYPE: DNA
```

i ORGANISM: Homo sapiens  
US-10-163-866-33

Query Match 55.0%; Score 1454.4; DB 14; Length 1542;  
Best Local Similarity 96.5%; Pred. No. 0;  
Matches 1519; Conservative 0; Mismatches 1; Indels 54; Gaps 1;  
QY 182 GAAAGCCTGTGTGCTCCACCATCTCCAAAGAGGTTACCTGCAGGGAAATGTTAAACGGGA 241  
Db 16 GAAAGCCTGTGTGCTCCACCATCTCCAAAGAGGTTACCTGCAGGGAAATGTTAAACGGGA 75  
QY 242 GCGTGCCTTCCCTGGGCAACAGAGGCCACTGGGAGGACGCTTTTCAGGAAGAGACG 301  
Db 76 GCGTGCCTTCCCTGGGCAACAGAGGCCACTGGGAG----- 113  
QY 302 CTTTTTCAGGAAGAGCGCCCTTTTCAGGAAGAGAGAGTGCAGCTGAAGAGAAAGTCA 361  
Db 114 -----GAGAAAGTGCAGCTCAAGAGAAAGTCA 141  
QY 362 CTTTACTGAGGGAGTCTCCATTATCATTTGGCCACCATTCATTGGAGCAGGAATCTTTCATCT 421  
Db 142 CTTTACTGAGGGAGTCTCCATTATCATTTGGCCACCATTCATTGGAGCAGGAATCTTTCATCT 201  
QY 422 CTCTTAAGGCGTGTCTCCAGAAACAGGGAGCGTGGGCATGTCTCTGAACATCTGGACGG 481  
Db 202 CTCTTAAGGCGTGTCTCCAGAAACAGGGAGCGTGGGCATGTCTCTGAACATCTGGACGG 261  
QY 482 TGTGTGGGTCCTGTCACATATTTTGGAGCTTGTCTTATGCTGAATTTGGGAACAACATATA 541  
Db 262 TGTGTGGGTCCTGTCACATATTTTGGAGCTTGTCTTATGCTGAATTTGGGAACAACATATA 321  
QY 542 AGAAATCTGGAGTCAATACATATATTTTGAAGTCTTTTGGTCCATTACCAAGCTTTTG 601  
Db 322 AGAAATCTGGAGTCAATACATATATTTTGAAGTCTTTTGGTCCATTACCAAGCTTTTG 381  
QY 602 TAGGAGTCTGGTGGAACTCTCATTAATAGCCCTCGAGTACTGCTGTGATATCCCTGG 661  
Db 382 TAGGAGTCTGGTGGAACTCTCATTAATAGCCCTCGAGTACTGCTGTGATATCCCTGG 441  
QY 662 CATTTGGAGCTACATCTTGGAGCACTTTTATTCATGTAAGTGAATCCCTGAACTTGGCA 721  
Db 442 CATTTGGAGCTACATCTTGGAGCACTTTTATTCATGTAAGTGAATCCCTGAACTTGGCA 501  
QY 722 TCAAGTCAATACAGCTGTGGGCAATCACTGATGATGCTCTCAATAGCATGAGTCA 781  
Db 502 TCAAGTCAATACAGCTGTGGGCAATCACTGATGATGCTCTCAATAGCATGAGTCA 561  
QY 782 GCTGGAGCCCGGATCCAGATTTCTTAACCTTTTGAAGCTCAAGCAATCTGATATA 841  
Db 562 GCTGGAGCCCGGATCCAGATTTCTTAACCTTTTGAAGCTCAAGCAATCTGATATA 621  
QY 842 TTATAGTCCCTGGAGTTATGCAAGTAAATTAAGTCAAAAGCAGAACTTTAAAGAGCCT 901  
Db 622 TTATAGTCCCTGGAGTTATGCAAGTAAATTAAGTCAAAAGCAGAACTTTAAAGAGCCT 681  
QY 902 TTTTCAAGAGAGATTCAAGTATACCGGTTGCCACTGGCTTTTATATGGAATGATG 961  
Db 682 TTTTCAAGAGAGATTCAAGTATACCGGTTGCCACTGGCTTTTATATGGAATGATG 741  
QY 962 CATATGCTGGCTGTTTACCTCACTTTGTTACTGAAGAGTAGAATCCCTGAAAAA 1021  
Db 742 CATATGCTGGCTGTTTACCTCACTTTGTTACTGAAGAGTAGAATCCCTGAAAAA 801  
QY 1022 CCATTCCTCTTCAATATGATATCATGGCCATTGTCACCATTTGGCTATGCTGACAA 1081  
Db 802 CCATTCCTCTTCAATATGATATCATGGCCATTGTCACCATTTGGCTATGCTGACAA 861  
QY 1082 ATGTGGCTCTTTACGACATTAATGCTGAGAGCTGCTGCTTTCAATGCAAGTGGCAG 1141  
Db 862 ATGTGGCTCTTTACGACATTAATGCTGAGAGCTGCTGCTTTCAATGCAAGTGGCAG 921  
QY 1142 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTATTAGCATTCGATCTTTGTTGCC 1201

## RESULT 14

US-10-163-866-52  
; Sequence 52, Application US/10163866  
; Publication No. US20030027188A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-080C  
; CURRENT APPLICATION NUMBER: US/10/163,866  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/338,733  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/357,600  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 52  
; LENGTH: 1528  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-163-866-52

Query Match 63.9%; Score 1431.8; DB 14; Length 1528;  
Best Local Similarity 96.4%; Pred. No. 0;

Matches 1497; Conservative 0; Mismatches 2; Indels 54; Gaps 1;									
Qy	182	GAAGCCCTGTTGTGTCACCATCTCCAAAGAGAGTTACCTGACAGGAATGTTAAACGGGA	241						
Db	30	GAAGCCCTGTTGTGTCACCATCTCCAAAGAGAGTTACCTGACAGGAATGTTAAACGGGA	89						
Qy	242	GGCTGCTTCCCTGGGCAACAGGAGCCACCTGGGACGACGCCCTTTTCAGGAAGAGACG	301						
Db	90	GGCTGCTTCCCTGGGCAACAGGAGCCACCTGGGACG	127						
Qy	302	CTTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTGACGCTGAAGAGGAAGTCA	361						
Db	128	-----GAGAAAGTGACGCTGAAGAGGAAGTCA	155						
Qy	362	CTTTACTGAGGGAGTCTCCATTATCATTTGGCACCATTATGGAGCAGGAATCTTCATCT	421						
Db	156	CTTTACTGAGGGAGTCTCCATTATCATTTGGCACCATTATGGAGCAGGAATCTTCATCT	215						
Qy	422	CTCTTAAGGGCGTGCTCCAGAACACGGGACGGTGCGCATGCTCTGACCATCTGGACGG	481						
Db	216	CTCTTAAGGGCGTGCTCCAGAACACGGGACGGTGCGCATGCTCTGACCATCTGGACGG	275						
Qy	482	TGCTGGGCTCCTCTCACTATTTGGAGCTTTTGGAGTCTTTGGTCCATTACGAGCTTTTG	541						
Db	276	TGCTGGGCTCCTCTCACTATTTGGAGCTTTTGGAGTCTTTGGTCCATTACGAGCTTTTG	335						
Qy	542	AGAAATCTGGAGGTCATTACACATATATTTGGAGTCTTTGGTCCATTACGAGCTTTTG	601						
Db	336	AGAAATCTGGAGGTCATTACACATATATTTGGAGTCTTTGGTCCATTACGAGCTTTTG	395						
Qy	602	TACGAGTCTGGTGGAATCTCTAATAACGCCCTGCAGCTACTGCTGTATATCCCTGG	661						
Db	396	TACGAGTCTGGTGGAATCTCTAATAACGCCCTGCAGCTACTGCTGTATATCCCTGG	455						
Qy	662	CATTGGAGCGTACATCTGGAACCATTTTATTCATGTAATGTAATCCCTGGAATGGCA	721						
Db	456	CATTGGAGCGTACATCTGGAACCATTTTATTCATGTAATGTAATCCCTGGAATGGCA	515						
Qy	722	TCAAGCTCATTACAGCTGTGGGCACTAAGTGTAGTGTGCTTAAATAGCATGAGTGCA	781						
Db	516	TCAAGCTCATTACAGCTGTGGGCACTAAGTGTAGTGTGCTTAAATAGCATGAGTGCA	575						
Qy	782	GCTGGAGCGCCGATCCAGATTTCTTAACTTTTGAAGCTCACAGCAATCTGTATAA	841						
Db	576	GCTGGAGCGCCGATCCAGATTTCTTAACTTTTGAAGCTCACAGCAATCTGTATAA	635						
Qy	842	TTATAGTCCCTGGAGTATGAGCTAATTAAGGTCACACGAGCTTTAAAGACGCT	901						
Db	636	TTATAGTCCCTGGAGTATGAGCTAATTAAGGTCACACGAGCTTTAAAGACGCT	695						
Qy	902	TTTCAGGAAGAGATTCAGATTTACGCGGTTGCCACTGGCTTTTATTCGGAATGTATG	961						
Db	696	TTTCAGGAAGAGATTCAGATTTACGCGGTTGCCACTGGCTTTTATTCGGAATGTATG	755						
Qy	962	CATATGCTGGCTGTTTACTCAACTTTGTTACTGAAGAGTAGAAAACCTGAAAAA	1021						
Db	756	CATATGCTGGCTGTTTACTCAACTTTGTTACTGAAGAGTAGAAAACCTGAAAAA	815						
Qy	1022	CCATTCCCTTGCATATGATATCCATGGCCATGTCACCATGGCTATGCTGACAA	1081						
Db	816	CCATTCCCTTGCATATGATATCCATGGCCATGTCACCATGGCTATGCTGACAA	875						
Qy	1082	ATGTGGGCTACTTTACGACCAATTAATGCTGAGGAGTGTCTCTTTCAAATGCACTGGCAG	1141						
Db	876	ATGTGGGCTACTTTACGACCAATTAATGCTGAGGAGTGTCTCTTTCAAATGCACTGGCAG	935						
Qy	1142	TGACCTTTTCTGACGGCTACTGGGAAATTTCTCATTCAGAGTTCGCAATCTTTTGGCC	1201						
Db	936	TGACCTTTTCTGACGGCTACTGGGAAATTTCTCATTCAGAGTTCGCAATCTTTTGGCC	995						
Qy	1202	TCTCTGCTTTGGCTCCATGAAACGGTGCTGTGTTGCTGTCTCCAGGTATCTCATGTTG	1261						
Db	996	TCTCTGCTTTGGCTCCATGAAACGGTGCTGTGTTGCTGTCTCCAGGTATCTCATGTTG	1055						

RESULT 15  
US-10-163-866-34  
; Sequence 34, Application US/10163866  
; Publication No. US20030027188A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-080C  
; CURRENT APPLICATION NUMBER: US/10/163,866  
; PRIOR FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/338,733  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/357,600  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 34  
; LENGTH: 2000  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-163-866-34

Query Match 61.3%; Score 1373.4; DB 14; Length 2000;									
Best Local Similarity 96.0%; Pred. No. 0;									
Matches 1441; Conservative 0; Mismatches 6; Indels 54; Gaps 1;									
Qy	182	GAAGCCCTGTTGTGTCACCATCTCCAAAGAGAGTTACCTGACAGGAATGTTAAACGGGA	241						
Db	143	GAAGCCCTGTTGTGTCACCATCTCCAAAGAGAGTTACCTGACAGGAATGTTAAACGGGA	202						
Qy	242	GGCTGCTTCCCTGGGCAACAGGAGCCACCTGGGACGACGCCCTTTTCAGGAAGAGACG	301						
Db	203	GGCTGCTTCCCTGGGCAACAGGAGCCACCTGGGACG	240						



QY 302 CCTTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAGAGAGAAAGTCA 361  
Db 241 -----GAGAAAGTGCAGCTGAGAGAGAAAGTCA 268  
QY 362 CTTTACTGAGGGAGTCTCCATATATCATGGAACCATATTCGAGCAGGAATCTTCATCT 421  
Db 269 CTTTACTGAGGGAGTCTCCATATATCATGGAACCATATTCGAGCAGGAATCTTCATCT 328  
QY 422 CTCTTAAGGCGTGTCCAGAACAGGGCAGGGTGGCATGCTCTGACCATCTGGACG 481  
Db 329 CTCTTAAGGCGTGTCCAGAACAGGGCAGGGTGGCATGCTCTGACCATCTGGACG 388  
QY 482 TGTGTGGGTCTGTCTCATATTTGGAGCTTGTCTTATGCTGAATTTGGAAACAACTATAA 541  
Db 389 TGTGTGGGTCTGTCTCATATTTGGAGCTTGTCTTATGCTGAATTTGGAAACAACTATAA 448  
QY 542 AGAAATCTGGAGTCAATACATATATTTGGAGTCTTTGGTCCATTAACAGCTTTTG 601  
Db 449 AGAAATCTGGAGTCAATACATATATTTGGAGTCTTTGGTCCATTAACAGCTTTTG 508  
QY 602 TACGAGTCTGGGTGGAATCTCTATAATACGCCCTGCAGTACTGCTGTGATATCCCTGG 661  
Db 509 TACGAGTCTGGGTGGAATCTCTATAATACGCCCTGCAGTACTGCTGTGATATCCCTGG 568  
QY 662 CATTTGGAGCTACATTTCTGGAACCATTTTATTCGAATGCAATCCCTGAACCTGCGA 721  
Db 569 CATTTGGAGCTACATTTCTGGAACCATTTTATTCGAATGCAATCCCTGAACCTGCGA 628  
QY 722 TCAAGCTCATTAAGTCTGGGCAATACCTGTAGTGTGATGCTTAAATAGCATGAGTCA 781  
Db 629 TCAAGCTCATTAAGTCTGGGCAATACCTGTAGTGTGATGCTTAAATAGCATGAGTCA 688  
QY 782 GCTGAGCGCCGCGATCCAGATTTCTTAAACCTTTTGAAGCTCACAGCAATCTTGATAA 841  
Db 689 GCTGAGCGCCGCGATCCAGATTTCTTAAACCTTTTGAAGCTCACAGCAATCTTGATAA 748  
QY 842 TTATAGTCCCTGGAGTTATGCAAGTCAATTAAGTCAACGAGCAATTTTAAAGCGGCT 901  
Db 749 TTATAGTCCCTGGAGTTATGCAAGTCAATTAAGTCAACGAGCAATTTTAAAGCGGCT 808  
QY 902 TTTTCAGGAGAGATTCAAGTATACGGGTGCGCATGCTGCTTTTATATGGAATGTATG 961  
Db 809 TTTTCAGGAGAGATTCAAGTATACGGGTGCGCATGCTGCTTTTATATGGAATGTATG 868  
QY 962 CATATGCTGGCTGGTTTACCTCAACTTTGTACTGAGAAAGTGAAGCAACCTGAAABAA 1021  
Db 869 CATATGCTGGCTGGTTTACCTCAACTTTGTACTGAGAAAGTGAAGCAACCTGAAABAA 928  
QY 1022 CCAITCCCTTGCATATATGATATCAATGGCCATTTGACCAATGGCTATGTGCTGACAA 1081  
Db 929 CCAITCCCTTGCATATATGATATCAATGGCCATTTGACCAATGGCTATGTGCTGACAA 988  
QY 1082 ATGTGGCTACTTTACGACCATATATGCTGAGGAGTCTGCTTTCAATGAGTGGGAG 1141  
Db 989 ATGTGGCTACTTTACGACCATATATGCTGAGGAGTCTGCTTTCAATGAGTGGGAG 1048  
QY 1142 TGACCTTTTCTGAGCGGTACTGGAATTTCTCATTAGCAGTCTCCGATCTTTGTTGCC 1201  
Db 1049 TGACCTTTTCTGAGCGGTACTGGAATTTCTCATTAGCAGTCTCCGATCTTTGTTGCC 1108  
QY 1202 TCTCTGCTTTGGCTCCAGAACGCTGTGTGTTGCTGTCTCCAGGTTATTTCTATGTTG 1261  
Db 1109 TCTCTGCTTTGGCTCCAGAACGCTGTGTGTTGCTGTCTCCAGGTTATTTCTATGTTG 1168  
QY 1262 CGTCTCGAGAGGTCACCTCCAGAAATCCCTCCATGATTCATGTCGCGAGCACTC 1321  
Db 1169 CGTCTCGAGAGGTCACCTCCAGAAATCCCTCCATGATTCATGTCGCGAGCACTC 1228  
QY 1322 CTCTACAGCTGTATTTGTTGACCCCTTTGACAAATGATATGCTCTTCTGAGACC 1381  
Db 1229 CTCTACAGCTGTATTTGTTGACCCCTTTGACAAATGATATGCTCTTCTGAGACC 1288

QY 1382 TCGACAGTCTTTTGAATTTTCTCAGTTTTCAGAGTGGCTTTTATTTGGGCTGGAGTTG 1441  
Db 1289 TCGACAGTCTTTTGAATTTTCTCAGTTTTCAGAGTGGCTTTTATTTGGGCTGGAGTTG 1348  
QY 1442 CTGGGCTGATTTATCTTTCGATACAAATGCCAGATATGCATCGTCTTTCAGAGTGGCAC 1501  
Db 1349 CTGGGCTGATTTATCTTTCGATACAAATGCCAGATATGCATCGTCTTTCAGAGTGGCAC 1408  
QY 1502 TGTTCATCCAGCTTTGTTTTCCTTTCATGCTCTTCATGCTGCTTCCCTTCCCTCTATT 1561  
Db 1409 TGTTCATCCAGCTTTGTTTTCCTTTCATGCTCTTTCATGCTGCTTCCCTTCCCTCTATT 1468  
QY 1562 CGGACCCATTTAGTACAGGGATTTGGCTTTCGTCATCACTCTGACTGGAGTCCCTGCTATT 1621  
Db 1469 CGGACCCATTTAGTACAGGGATTTGGCTTTCGTCATCACTCTGACTGGAGTCCCTGCTATT 1528  
QY 1622 ATCTCTTTATATATGGGACAAAGAACCCAGGTGCTTTAGATAATATGTCAGAGAAATAA 1681  
Db 1529 ATCTCTTTATATATGGGACAAAGAACCCAGGTGCTTTAGATAATATGTCAGAGTTCCCTAG 1588  
QY 1682 C 1682  
Db 1589 C 1589

Search completed: October 30, 2003, 07:34:09  
Job time : 1069 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 31, 2003, 10:50:02 ; Search time 38.5 seconds

(without alignments)  
4921.247 Million cell updates/sec

Title: US-09-667-170A-440

Perfect score: 4120

Sequence: 1 ggaggttgagtgagcagag.....ttattataaaaaaaaaaaaaa 2239

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-USER=US09667170 @CGN 1.1 50 @runat 31102003 104951 10380 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREAS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:  
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3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1156.5	28.1	515	2	US-09-073-362-3
2	1156.5	28.1	515	2	US-09-243-920-3
3	1131.5	27.5	511	2	US-09-073-362-1
4	1131.5	27.5	511	2	US-09-243-920-1
5	741.5	18.0	352	4	US-09-489-847-255
6	730	17.7	370	4	US-09-489-847-127
7	621	15.1	241	2	US-08-825-781-3
8	615	14.9	241	2	US-08-825-781-4
9	537.5	13.0	525	4	US-09-107-532A-5743
10	524.5	12.7	245	2	US-08-825-781-1
11	417.5	11.5	417	4	US-09-107-532A-4001
12	286	6.9	629	2	US-08-132-990A-8

13	286	6.9	629	5	PCT-US92-09382-8
14	282.5	6.9	521	4	US-09-134-001C-4290
15	279.5	6.8	622	2	US-08-132-990A-4
16	279.5	6.8	622	5	PCT-US92-09382-4
17	261	6.3	485	4	US-09-252-991A-32881
18	259.5	6.3	421	4	US-09-107-532A-4030
19	257	6.2	484	4	US-09-252-991A-32299
20	244	5.9	453	4	US-09-328-352-4181
21	237.5	5.8	454	4	US-09-252-991A-30013
22	237.5	5.8	484	4	US-09-328-352-6041
23	235	5.7	494	4	US-09-328-352-7016
24	232.5	5.6	505	4	US-09-328-352-7155
25	232.5	5.6	672	4	US-09-556-916-26
26	232.5	5.6	672	4	US-09-556-916-28
27	231.5	5.6	462	4	US-09-328-352-6483
28	231.5	5.6	486	4	US-09-252-991A-31847
29	229.5	5.6	489	4	US-09-328-352-5330
30	229	5.6	508	4	US-09-328-352-6467
31	226.5	5.5	534	4	US-09-328-352-6713
32	224.5	5.4	499	4	US-09-134-001C-5370
33	222	5.4	586	4	US-09-252-991A-24994
34	221	5.4	510	4	US-09-252-991A-26663
35	216	5.2	445	4	US-09-328-352-6669
36	213.5	5.2	480	4	US-09-252-991A-18961
37	212.5	5.2	482	4	US-09-328-352-6084
38	211.5	5.1	472	4	US-09-352-991A-18544
39	211.5	5.1	525	4	US-09-352-991A-21543
40	210	5.1	472	4	US-09-328-352-4537
41	209.5	5.1	477	4	US-09-252-991A-29825
42	208.5	5.1	481	4	US-09-252-991A-27157
43	205	5.0	484	4	US-09-328-352-4849
44	204	5.0	464	4	US-09-252-991A-27800
45	202	4.9	488	4	US-09-328-352-4928

#### ALIGNMENTS

##### RESULT 1

US-09-073-362-3  
; Sequence 3, Application US/09073362  
; Patent No. 5942399  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Coxley, Neil C.  
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073,362  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carrone, Michael C  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0514 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166







STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/243,920  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/073,362  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cerrone, Michael C  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PF-0514 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 511 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: ESOGTUT02  
 CLONE: 2667831

US-09-243-920-1

## Alignment Scores:

Pred. No.: 4,15e-110 Length: 511  
 Score: 1131.50 Matches: 214  
 Percent Similarity: 68.00% Conservative: 109  
 Best Local Similarity: 45.05% Mismatches: 149  
 Query Match: 27.46% Indels: 3  
 DB: 2 Gaps: 2

US-09-667-170A-440 (1-2239) x US-09-243-920-1 (1-511)

QY 310 GGAAGACGCCCTTTTCAGGAGAGAGAACTGACGCTGAGAGAGAACTCACTTTACTG 369  
 Db 21 GlyAspGlyAlaSerProGlyProGluGlnValLysLeuLysGluLeuSerLeuLeu 40  
 QY 370 AGGGAGCTCCATTATCATTTGCGACCATCATTTGGAGCAGGAATCTTCATCTCCCTAAG 429  
 Db 41 AsnGlyValCysLeuLeuValGlyAsnMetIleGlySerGlyIlePheValSerProLys 60  
 QY 430 GGCGTGCTCCAGAACACGGGACGGTGGCGATGCTCTGACCACTCGACGGTGTTGGG 489  
 Db 61 GlyValLeuIleTyrSerAlaSerPheGlyLeuSerLeuValIleTyrAlaValGlyGly 80  
 QY 490 GTCTGTGCTATTTGGAGCTTGTCTATGCTGAATGGGAACATATAAGAAATCT 549  
 Db 81 LeuPheSerValPheGlyAlaLeuCysTyrAlaGluLeuGlyThrThrIleLysSer 100  
 QY 550 GGAGGTCAATACATATATTTGGAGTCTTGTGTCATTCACCATTCACGCTTTTGTACGAGTC 609  
 Db 101 GlyAlaSerTyrAlaTyrIleLeuGluAlaPheGlyGlyPheLeuAlaPheIleArgLeu 120  
 QY 610 TGGGTGGAACCTTCATAATACGCCCTGACACTGCTGTGATATCCCTGGCATTTTGA 669  
 Db 121 TrpThrSerLeuLeuIleIleGluProThrSerGlnAlaIleIleAlaIleThrPheAla 140  
 QY 670 CGCTACATTCGGAACCACTTTTATTCAATGTAATCCCTGAACTTGGCATCAAGCTC 729  
 Db 141 AsnTyrMetValGlnProLeuPheProSerCysPheAlaProTyrAlaAlaSerArgLeu 160

## RESULT 5

US-09-489-847-255

; Sequence 255, Application US/09489847

; Patent No. 6476195

QY 730 ATTACAGCTGTGGCATAAAGTGTAGTGTGCTCTAAATAGCATGAGTGTACAGCTGAGC 789  
 Db 161 LeuAlaAlaCysIleCysLeuLeuThrPheIleAsnCysAlaTyrValLysTrpGly 180  
 QY 790 GCCGGATCCAGATTTTCTTAACCTTTTGCAGCTCACAGCAATTTCTGATAATATAGTC 849  
 Db 181 ThrLeuValGlnAspIlePheThrTyrAlaLysValLeuAlaLeuIleAlaValIleVal 200  
 QY 850 CTGGAGTTATGCGCTAATTAAGGTCAACCCAGAACCTTTAAAGCCGCTTTTCAGGA 909  
 Db 201 AlaGlyIleValArgLeuGlyGlnGlyAlaSerThrHisPheGluAsnSerPheGluGly 220  
 QY 910 AGAGATTCAAGTATTACGGGTTTGCACCTGGCTTTTATTATGGAATGATGATATGCT 969  
 Db 221 SerSerPheAlaValGlyAspIleAlaLeuAlaLeuTyrSerAlaLeuPheSerTyrSer 240  
 QY 970 GGCTGTTTTTACCTCAACTTTGTACTGAAGTAGAAGAACCCCTGAAAAACCATTCOC 1029  
 Db 241 GlyTyrAspThrLeuAsnTyrValThrGluGluIleLysAsnProGluArgAsnLeuPro 260  
 QY 1030 CTTCGAATATGATATCCATGGCCATGTCCACATTTGGCTATGCTGACAAATGGGCC 1089  
 Db 261 LeuSerIleGlyIleSerMetProIleValThrIleIleTyrIleLeuThrAsnValAla 280  
 QY 1090 TACTTTACGACCATTAATGCTGAGGAGCTGCTCTTTCAATGACGTGGCAGTACCTTT 1149  
 Db 281 TyrTyrThrValLeuAspMetArgAspIleLeuAlaSerAspAlaValAlaValThrPhe 300  
 QY 1150 TCTGAGCGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTCCTCTCTGTC 1209  
 Db 301 AlaAspGlnIlePheGlyIlePheAsnTyrIleIleProLeuSerValAlaLeuSerCys 320  
 QY 1210 TTTGGCTCCATGAAACGGTGTGTTGCTGCTCCAGGTATTCTATGTTGGTCTCGA 1269  
 Db 321 PheGlyGlyLeuAsnAlaSerIleValAlaAlaSerArgLeuPheValGlySerArg 340  
 QY 1270 GAGGTCACCTTCCAGAAATCTCTCCATGATTCATGTCGCGACGACACACTCTCTACCA 1329  
 Db 341 GluGlyHisLeuProAspAlaIleCysMetIleHisValGluArgPheThrProValPro 360  
 QY 1330 GCTGTTATGTTTGCACCCCTTTGCAATGATAATCTCTCTCTGAGACCTCGACAGT 1389  
 Db 361 SerLeuLeuPheAsnGlyIleMetAlaLeuIleTyrLeuCysValGluAspIlePheGln 380  
 QY 1390 CTTTTCGATTTCTCAGTTTTCAGCTGCTTTTATTTGGCTGGCAGTTGCTGGCTG 1449  
 Db 381 LeuIleAsnTyrTyrSerPheSerTyrTyrPhePheValGlyLeuSerIleValGlyGln 400  
 QY 1450 ATTTATCTTCGATACAAATGCCAGATATGCACTGCTCTTCAAGGTGCCACGTTCATC 1509  
 Db 401 LeuTyrLeuArgTrpLysGluProAspArgProArgProLeuLysLeuSerValPhePhe 420  
 QY 1510 CCAGCTTTGTTTTCCTCATGCTCTCTCATGTTGCCCTTTCCCTCTATTCGGACCCA 1569  
 Db 421 ProIleValPheCysLeuCysThrIlePheLeuValAlaValProLeuTyrSerAspThr 440  
 QY 1570 TTTAGTACAGGATTCGGCTTCGTCATCACTCTGACGTGGAGTCCCTCGGTATATCTTT 1629  
 Db 441 IleAsnSerLeuIleGlyIleAlaIleAlaLeuSerGlyLeuProPheTyrPheLeuIle 460  
 QY 1630 ATT-----ATATGGACCAAGAACCCAGGTGGTGTAGGAATAATGTCCAGAAAAATAACC 1683  
 Db 461 IleArgValProGluHisLysArgProLeuTyrLeuArgIleValGlySerAlaThr 480  
 QY 1684 AGAACATTACAAATAATA---CTGGAAGTTGTACCAAGAAAGAT 1725  
 Db 481 ArgTyrLeuGlnValLeuCysMetSerValAlaAlaGluMetAsp 495

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 255
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-489-847-255

Alignment Scores:
Pred. No.: 376 Length: 352
Score: 741.50 Matches: 140
Percent Similarity: 66.67% Conservative: 84
Best Local Similarity: 41.67% Mismatches: 109
Query Match: 18.00% Indels: 3
DB: 4 Gaps: 2

US-09-667-170A-440 (1-2239) x US-09-489-847-255 (1-352)

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Db 1 LeuLeuAlaAlaCysIleCysLeuLeuThrPheIleAenCysAlaTyValIleTyr 20

Qy 787 AGCGCCGGATCCAGATTTCTTAACTTTGCAAGCTCAGCAATTTCTGATATATA 846
Db 21 GlyThrLeuValGlnAspIlePheThrTyAlaLysValLeuAlaLeuIleAlaValle 40

Qy 847 GTCCCTGAGTATGACCTATTAAGCTCAAGCGAAGACTTAAAGCGCTTTTCA 906
Db 41 ValAlaGlyIleValArgLeuGlyGlnGlyAlaSerThrHisPheGluAsnSerPheGlu 60

Qy 907 GGAAGAGATTCAAGTATTACCGGTTGCCACTGCTTTTATTATGGAATGATGATAT 966
Db 61 GlySerPheAlaValGlyAspIleAlaLeuAlaLeuTySerAlaLeuPheSerTy 80

Qy 967 GCTGGCTGTTTACCTCACTTTGTTACTGAAGTAGAAGAACCCCTGAAAGAACCAT 1026
Db 81 SerGlyTyrPheThrLeuAsnTyValThrGluGluIleLysAsnProGluArgAsnLeu 100

Qy 1027 CCCCTTCAATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1086
Db 101 ProLeuSerIleGlyIleSerMetProLeuValThrIleLeuIleLeuThrAsnVal 120

Qy 1087 GCCTACTTACGACCAATTAATGCTGAGGAGTGTGCTTTCAATGACGAGTGGAGTGCAC 1146
Db 121 AlaTyTyThrValLeuAspMetArgAspIleLeuAlaSerAspAlaValAlaValThr 140

Qy 1147 TTTTCTGAGCGGCTACTGGGAAATTTCTCAATAGCATGTCGATCTTTGTCCTCTCC 1206
Db 141 PheAlaAspGlnIlePheGlyIlePheAsnTrpIleLeuProLeuSerValAlaLeuSer 160

Qy 1207 TGCTTTGCTCCAGAGCGGTGGTGTGCTGCTCTCCAGGTATTCATGTTGCTGCTCT 1266
Db 161 CysPheGlyGlyLeuAsnAlaSerIleValAlaAlaSerArgLeuPhePheValGlySer 180

Qy 1267 CGAGAGGCTCACCTTCCAGAAATCCTCTCCATGATTCTATGTCGCGAAGCACACTCTCTA 1326

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Db 201 ProSerLeuLeuPheAsnGlyIleMetAlaLeuIleTyLeuCysValGluAspIlePhe 220
Qy 1387 AGTCTTTGAATTTCCCTCAGTTTCCAGGTTGGCTTTTATTGGCTGGCAGTTGCTGG 1446
Db 221 GlnLeuLeuAsnTyTySerPheSerTyTrpPheValGlyLeuSerIleValGly 240
Qy 1447 CTGATTTATCTTCATACAAATGCCAGATATGATGCTCTCTTCAAGGTGCCACTGTC 1506
Db 241 GlnLeuTyLeuArgTrpLysGluProAspArgProArgProLeuLysLeuSerValPhe 260
Qy 1507 ATCCAGCTTTGTTTCTTCCATGCTCTTACATGCTCTTACATGCTTCCCTTCCCTTATTCGAC 1566
Db 261 PheProLeuValPheCysLeuCysThrIlePheLeuValAlaValProLeuTySerAsp 280
Qy 1567 CCATTAGTACAGGATTTGCTTCTGCTCATCATCTGCTGAGTCCCTGCGTATTATCTC 1626
Db 281 ThrIleAsnSerLeuIleGlyIleAlaIleAlaLeuSerGlyLeuProPheTyPheLeu 300
Qy 1627 TTTATT-----ATATGGGACAAGAACCCAGGTGTTTACATAATGTCAGAGAAATA 1680
Db 301 IleIleArgValProGluHisLysArgProLeuTyLeuArgGlyIleValGlySerAla 320
Qy 1681 ACCAGAACATTACAAATAATA---CTGGAAGTTGTACCAAGAAAGAT 1725
Db 321 ThrArgTyLeuGlnValLeuCysMetSerValAlaAlaGluMetAsp 336

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## RESULT 6

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US-09-489-847-127
; Sequence 127, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 127
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (370)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-127

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Alignment Scores:
Pred. No.: 6,17e-68 Length: 370
Score: 730.00 Matches: 140
Percent Similarity: 63.76% Conservative: 87
Best Local Similarity: 39.33% Mismatches: 102
Query Match: 17.72% Indels: 27
DB: 4 Gaps: 3

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US-09-667-170A-440 (1-2239) x US-09-489-847-127 (1-370)

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9	Db	Ser	LeuLeuLeuLeuAlaAlaAlaCysIleCysLeuLeuThrPheIleAsnCysAlaTyr	28
778	QY	GT	CAGCTGGAGCGCGGATCCAGATTTTCCTAACTTTTCCAGCTCCACAGCAATCTG	837
29	Db	Val	LeuValGlnAspIlePheThrTyrAlaIleValLeuAlaLeuLeu	48
838	QY	ATA	TATATAGTCCCTGGAGTTATCGAGCTAAATTAAGCTCAACCGCAGAACTTTAAAGAC	897
49	Db	Ala	ValIleValAlaGlyIleValArgLeuGlyGlnGlyAlaSerThrHisPheGluAsn	68
898	QY	GC	CTTTTTCAGGAAGAGATTCAGGTATTACGGGTGCCACCTGGCTTTTATTATGGAATG	957
69	Db	Ser	PheGluGlySerSerPheAlaValGlyAspIleAlaLeuTyrSerAlaLeu	88
958	QY	TAT	GCATATGCTGGCTGGTTTAACTCAACATTTCTTACTGAAGAAGTAGAAAAACCTGAA	1017
89	Db	Phe	SerTyrSerGlyTyrAspThrLeuAsnTyrValThrGluGlnIleLysAsnProGlu	108
1018	QY	AAA	ACCATTCCTGCAATATGATATCCATGCGCATTTGCACCATTTGGCTATGTCGCT	1077
109	Db	Arg	AsnLeuProLeuSerIleGlyIleSerMetProIleValThrIleIleTyrIleLeu	128
1078	QY	ACA	AATGTGCGCTACTTTAGACCATTAATGCTGAGGAGCTGCTCTTCAAATGCGATG	1137
129	Db	Thr	AsnValAlaTyrTyrThrValLeuAspMetArgAspIleLeuAlaSerAspAlaVal	148
1138	QY	GC	AGTGCATTTCTGAGCGGCTACTCGGAAATTTCTCATTTAGCAGTTCGCAATCTTGT	1197
149	Db	Ala	ValThrPheAlaAspGlnIlePheGlyIlePheAsnTrpIleIleProLeuSerVal	168
1198	QY	GC	CTCTCTCTGCTTTGGCTCCATGAACGGTGGTGTGTGCTGCTCCAGTATTCTCAT	1257
169	Db	Ala	LeuSerCysPheGlyGlyLeuAsnAlaSerIleValAlaAlaSerArgLeuPhePhe	188
1258	QY	GT	TGCGTCTCGAGAGGCTCACTTCCAGAATCTCTCCATGATTCATGCCGACACAC	1317
189	Db	Val	GlySerArgGluGlyHisLeuProAspAlaIleCysMetIleHisValGluArgPhe	208
1318	QY	ACT	CTCTACCACTGTATTGTTTTCACCCCTTGACATGATATGCTCTCTCTCTGGA	1377
209	Db	Thr	ProValProSerLeuLeuPheAsnGlyIleMetAlaLeuIleTyrLeuCysValGlu	228
1378	QY	GAC	CTCGACAGTCTTTGAATTTCTCAGTTTTCGACAGTGGCTTTTATTGGCTGGCA	1437
229	Db	Asp	IlePheGlnLeuIleAsnTyrTyrSerPheSerTyrTrpPheValGlyLeuSer	248
1438	QY	GT	TGCTGGGTGATTATCTTCGATACAAATGCCAGATATGATCTCTCTTCAAGTG	1497
249	Db	Ile	ValGlyGlnLeuTyrLeuArgTrpLysGluProAspArgProArgProLeuLysLeu	268
1498	QY	CCA	TGTTTCATCCAGCTTTGTTTTCCTTCACATGCTCTTCATGGTGGCTTCCCTC	1557
269	Db	Ser	ValPhePheProIleValPheCysLeuCysThrIlePheLeuAlaValProLeu	288
1558	QY	TAT	CGGACCAATTTAGTACAGGATTTGCTTCATCTCATCTCGATGGAGTCCCTCGC	1617
289	Db	Tyr	SerAspThrIleAsnSerLeuIleGlyIleAlaIleAlaLeuSerGlyLeuProPhe	308
1618	QY	TAT	TACTCTTTTATTATATCGGACAGAAACCCAGGTGGTTTGAATAATGTGCAGAGAA	1677
309	Db	Tyr	PheLeuIleIle-----ProLeuTyrLeuArg-----Arg	314
1678	QY	ATA	ACCAACATTAACAATAATACTGGAAGTTGTACCAAGAAGATAGTTATGAACT	1737
315	Db	Val	ProGluHisLysArg-----ProLeuTyrLeuArg-----	325
1738	QY	AAT	GGAAGTGTGGCAATCTGCCCAAGGGGAGACACAAAAT	1783
326	Db	Arg	SerTrpGlyLeuProGlnGlyThrSerArgSer	333

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RESULT 7
US-08-825-781-3
; Sequence 3, Application US/08825781
; Patent No. 5843727
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN TUMOR-ASSOCIATED MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,781
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0262 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 392990
US-08-825-781-3

Alignment Scores:
Pred. No.: 1,45e-56 Length: 241
Score: 621.00 Matches: 114
Percent Similarity: 68.49% Conservative: 49
Best Local Similarity: 47.90% Mismatches: 75
Query Match: 15.07% Indels: 0
DE: 2 Gaps: 0

US-09-667-170A-440 (1-2239) x US-08-825-781-3 (1-241)
QY 1009 AACCTTGAAAAACCAATTCCTCCGATATGATATCCATGGCCATTGCTGTC
Db 3 AsnProTyrArgAsnLeuProLeuAlaIleIleSerLeuProIleValT
QY 1069 TATGTCTCACAAATGTGGCCCTACTTTTACGACCATTAATGCTGAGGAGCTCG
Db .....
Db 23 TyrValLeuThrAsnLeuAlaTyrPheThrThrLeuSerThrAsnGlnMetL
QY 1129 ATGCGATGGCGAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTTCTCATTAG
Db .....
Db 43 GluAlaValAlaValAspPheGlyAsnTyrHisLeuGlyValMetSerTrpI
QY 1189 ATCTTTGTTCCTCTCCTGCTTTGGCTCCATGAACGGTGTGTGTTTGTGCTG
Db .....
Db 63 ValPheValGlyLeuSerCysPheGlySerValAsnGlySerLeuPheThrS

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QY 1249 TTATCTATGTCGCTCGAGGGTCACTTCAGAAATCCTCCATGATTCATGTC 1308
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 LeuPhePheValGlySerArgGluGlyHisLeuProSerIleLeuSerMetIleHisPro 102
QY CGAAGCACACTCTCTACAGCTGTATTTGTCACCCCTTGACAAATGATAATGCTC 1368
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
103 GlnLeuLeuThrProValProSerLeuValPheThrCysValMetThrLeuMetIleAla 122
QY TTCTCTGGAGACTCGACAGTCTTTGAATTCCTCAGTTTGGCAGGTGGCTTTTATT 1428
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 PheSerArgAspIlePheSerIleIleAsnPhePheSerPheAsnTrpLeuCysVal 142
QY GGCTGGCAGTCTCTGGGCTGTATTTCTTCGATACAAATGCCAGATGATGCTCT 1488
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
143 AlaLeuAlaIleIleGlyMetMetTrpLeuArgPheIleLeuAlaCysLeuPheLeuIleAla 162
QY TTCAAGTGGCCTATGTCATCCAGCTTTGTTTTCCTTCACATGCTCTTCATGTTGCC 1548
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
163 IleLysValAsnLeuAlaLeuProValPhePheIleLeuAlaCysLeuPheLeuIleAla 182
QY CTTTCCCTCTATTCGGACCCATTTAGTACAGGATTTGGCTTCGTCTCATCTGACTGGA 1608
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
183 ValSerPheTrpLysThrProLeuGluCysGlyIleGlyPheAlaIleLeuSerGly 202
QY GTCCCTGCGTATPATCTCTTTATATATGAGCAAGAAACCCAGGTGGTTTGAATAATG 1668
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
203 LeuProValTrpPhePheGlyValTrpTrpLysAsnLysProLysTrpIleLeuGlnVal 222
QY TCAGAGAAATACACAGACATTAACAATAACTCGAAGTGTACCAAGAA 1722
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223 IlePheSerValThrValLeuCysGlnLysLeuMetGlnValValProGlnGlu 240

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## RESULT 8

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US-08-825-781-4
; Sequence 4, Application US/08825781
; Patent No. 5843727
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN TUMOR-ASSOCIATED MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,781
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0262 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 181908
; US-08-825-781-4
; Alignment Scores:
; Pred. No.: 6,22e-56 Length: 241
; Score: 615.00 Matches: 115
; Percent Similarity: 68.07% Conservative: 47
; Best Local Similarity: 48.32% Mismatches: 76
; Query Match: 14.93% Indels: 0
; DB: 2 Gaps: 0
; US-09-667-170A-440 (1-2239) x US-08-825-781-4 (1-241)
QY 1009 AACCTGAAACCAACATCCCTTGCATATGATATATCCATGCCATTCACCATGGC 1068
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY TATGTCGTGACAAATGTCGCTACTTTACAGCATTAAATGCTGAGGAGCTGCTGTCA 1128
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 TyrValLeuThrAsnLeuAlaTrpPheThrThrLeuSerThrGluGlnMetLeuSer 42
QY AATGCAAGTGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATAGCAGTCCG 1188
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
43 GluAlaValAlaValAspPheGlyAsnTyrHisLeuGlyValMetSerTrpIleLeuPro 62
QY ATCTTTGTTGCCCTCTCCCTGCTTGGCTCCATGAGGGTGGTGTCTGCTCTCCAG 1248
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 ValPheValGlyLeuSerCysPheGlySerValAsnGlySerLeuPheThrSerSerArg 82
QY TTATCTATGTCGCTCGAGAGGCTCACCTTCCAGAAATCCTCCATGATTCATGTC 1308
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 LeuPhePheValGlySerArgGluGlyHisLeuProSerIleLeuSerMetIleHisPro 102
QY CGAAGCACACTCTCTACAGCTGTATTTGTTTCCACCCCTTGACAAATGATAATGCTC 1368
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
103 GlnLeuLeuThrProValProSerLeuValPheThrCysValMetThrLeuLeuTrpAla 122
QY TTCTCTGGAGACTCGACAGTCTTTTGAATTTCTCAGTTTGGCAGGTGGCTTTTATT 1428
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 PheSerLysAspIlePheSerValIleAsnPhePheSerPheAsnTrpLeuCysVal 142
QY GGCTGGCAGTCTCTGGGCTGTATTTATCTCGATACAAATGCCAGATGATGCTCTCT 1488
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
143 AlaLeuAlaIleIleGlyMetIleTrpLeuArgHisArgLysProGlnLeuGlnArgPro 162
QY TTCAGGTGGCCTGTTCATCCAGCTTTGTTTTCCTTCACATGCTCTTCATGTTGCC 1548
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
163 IleLysValAsnLeuAlaLeuProValPhePheIleLeuAlaCysLeuPheLeuIleAla 182
QY CTTTCCCTCTATTCGGACCCATTTAGTACAGGATTTGGCTTCGTCTCATCTGACTGGA 1608
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
183 ValSerPheTrpLysThrProValGluCysGlyIleGlyPheThrIleIleLeuSerGly 202
QY GTCCCTGCGTATPATCTCTTTATATGAGCAAGAAACCCAGGTGGTTTGAATAATG 1668
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
203 LeuProValTrpPhePheGlyValTrpTrpLysAsnLysProLysTrpIleLeuGlnGly 222
QY TCAGAGAAATACACAGACATTAACAATAACTCGAAGTGTACCAAGAA 1722
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
223 IlePheSerThrThrValLeuCysGlnLysLeuMetGlnValValProGlnGlu 240
; RESULT 9
; US-09-107-532A-5743
; Sequence 5743, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doncette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

```



NUMBER OF SEQUENCES: 7310  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02354

COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD-ROM ISO9660  
 COMPUTER: PC  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,532A  
 FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/085,598  
 FILING DATE: 14 May 1998  
 APPLICATION NUMBER: 60/051571  
 FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:  
 NAME: Ariniello, Pamela Deneke  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-012  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 5743:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 525 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHEICAL: YES  
 ORIGINAL SOURCE:  
 ORGANISM: Enterococcus faecium

FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (B) LOCATION 1...525  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5743:  
 US-09-107-532A-5743

Alignment Scores:  
 Pred. No.: 1.33e-47 Length: 525  
 Score: 537.50 Matches: 133  
 Percent Similarity: 48.58 Conservative: 106  
 Best Local Similarity: 27.03% Mismatches: 224  
 Query Match: 13.05% Indels: 29  
 Gaps: 4

US-09-667-170A-440 (1-2239) x US-09-107-532A-5743 (1-525)

QY 214 GGTACTGTGAGGAATGTTACGGAGGCTGCTTCCCTGGGCAACAAGGACCACT 273  
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 Db 39 GlyTyrVal---GlyLysThrGluArgLysileGlyArgAspGlylleGlnGluPro 57  
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 QY 274 GGGCAGGACGCTTT-----TCAGGAGA 297  
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 Db 58 HisProLysSerPheLeuTyrPheTyrAspTrpLeuTrpTyrGluArgGlyGlnGlyMet 77  
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 QY 298 GAGCGCTTTTCAGGAAGAGACGCTTTTCAGGAAGAGAGAAAGTCAGCTGAAGAGAAA 357  
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 Db 78 GluGluTyrGlnAlaThrProValLysGluValLysileGluAsnGluLeuLysArgThr 97  
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 QY 358 GTCACCTTACGAGGAGTCTCATTTATCATTCATGGCACCATTCATTGGACGAGAAATCTTC 417  
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 Db 98 MetGlyPhePheThrAlaLeuSerThrValMetGlyThrValLysileGlyAlaGlyValPhe 117  
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 QY 418 ATCTCTCTAAGGCGTCTCCCAACACGGGACGCTGGGACGTCTCTGACCACTGG 477  
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 Db 118 PheLysAlaAlaSerValAlaGluValThrGlySerAlaSerLeuHisMetPheSerTrp 137  
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QY 478 ACGTGTTGGGTCTCTGTCACATATTTGGAGCTTTGCTTATGCTGAATTTGGGAACAACT 537  
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 Db 138 PheLeuGlyGlyMetIleSerValCysAlaGlyLeuThrGlyAlaGluLeuAlaAla 157  
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 QY 538 ATAAAGAAATCTGGAGGTCAATACACATATTTTGAAGTCTTTGGTCCATTACCACT 597  
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 Db 158 IleProGluThrGlyGlyMetIleLysTyrIleGluArgIleIleGlyAsnThrAlaAla 177  
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 QY 598 TTGTACGAGTCTGGGTGGAACCTCTCATATAATACGCCCTCAGCTACTGCTGTATATCC 657  
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 Db 178 PheLeuLeuGlyTrpAlaGlnValIleIlePheProAlaAsnValAlaAlaLeuSer 197  
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 QY 658 CTGCGATTTGACGCTACATTTCTGGAACCACTTTTATTCAATGTGAAATCCCTGAACCT 717  
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 Db 198 IleIlePheGlyThrGlnPheValAsnLeuPhe-----GlyLeu 210  
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 QY 718 GCGATCAAGCTCAATTACAGCTGTGGGCATAAAGTGA-----GTGATGGTCTCTAAAT 768  
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 Db 211 SerGlnSerMetIleValProValAlaValThrAlaAlaValSerIleLeuLeuIleAsn 230  
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 QY 769 AGCATGAGTGTGAGTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTGCAGACTCACA 828  
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 Db 231 PheLeuGlySerLysAlaGlyAlaPheGlnSerIleThrLeuValCysLysLeuIle 250  
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 QY 829 GCAATTCGTGATAATTATAGCTCCCTGGAGTTATCAGCTAATTAAGGTCAACCGCAGAAC 888  
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 Db 251 ProLeuPheValIleValIlePheGlyLeuPheArgGlnGluGlyValAspPheGlnLeu 270  
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 QY 889 TTTAAAGACGCTTTTCAGGAAGAGATTCAAGTATTACGCGGTGTCACCTGGCTTTTAT 948  
 |||||  
 Db 271 PheProIleGlnAlaGlyGluAsnLeuSerPhePheSerAlaLeuGlyAlaGlyLeuLeu 290  
 |||||  
 QY 949 TATGGATGTATCATATGCTGCTGCTTTTACTCACTTCTTACTGAAGAGTAGAA 1008  
 |||||  
 Db 291 AlaThrMetPheAlaTyrAspGlyTrpIleHisValGlyAsnIleSerGlyGluLeuLys 310  
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 QY 1009 AACCTCTGAAAAAACCATTTCCCTTGCAATATGATATCATGCCATTGTCACCATTTGC 1068  
 |||||  
 Db 311 LysProAlaLysAspLeuProLysAlaIleSerLeuGlyIleIleGlyIleMetIleVal 330  
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 QY 1069 TATGCTGTGACAAATGTGCTTACTTACGACATTAATGCTGAGGAGCTGCTGCTTCA 1128  
 |||||  
 Db 331 TyrLeuLeuValAsnAlaValPheLeuArgThrAlaSerIleAspGlyValAlaGlyAsn 350  
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 QY 1129 AATGAGTGGCAGTGACCTTTCTGAGCGGCTACTCGGAAATTC---TCATTAGCAGTT 1185  
 |||||  
 Db 351 SerAsnAlaAlaSerAspValAlaLysMetIlePheGlyGlyPheGlyGlyArgLeuVal 370  
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 QY 1186 CCGATCTTTGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 1245  
 |||||  
 Db 371 ThrValGlyIleLeuIleSerValTyrGlyThrIleAsnGlyTyrThrLeuThrGlyMet 390  
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 QY 1246 AGTTATTCTATGTTCCGCTCTGAGAGGCTCACCTTCCA-----GAAATCCTCTCCATG 1299  
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 Db 391 ArgLeuProTyrValMetAlaLysGluAsnAsnLeuProPheSerLysLeuPheAlaLys 410  
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 QY 1300 ATTATGTCGCGAGCACACTCTCTACGAGCTGTTATGTTGTTGACCCCTTTGACAATG 1359  
 |||||  
 Db 411 LeuHisAspLysThrLysValProValAlaAlaGlyIleLeuGluLeuValIleAlaIle 430  
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 QY 1360 ATAATCTCTCTCTGAGACCTCGACAGCTTTTGAATTTCTCAGTTTTCAGGCTGG 1419  
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 Db 431 GlyMetMetIleGlyGlyPheAspThrLeuThrAspMetLeuIlePheValIleTrp 450  
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 QY 1420 CTTTTTATTTGGGTGGCAGTTGCTGGCTGATTTATCTTCGATACAAATGCCAGATATG 1479  
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 Db 451 IlePheTyrThrMetValPheValGlyValIleLeuLeuArgLysLysGluProAspLeu 470  
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 QY 1480 CATCGTCTCTCAAGTGGCAGCTG-----TTATCCAGCTTTGTTTCTTCACATGC 1533  
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 Db 471 PheArgProTyrLysValProMetTyrProPheIleProLeuValAlaIleIleGlyGly 490  
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 QY 1534 CTCCTCATGTTGGCTTTCCCTCTATTTCGGACCCATTTAGTACAGGGATTGGCTTCGTC 1593  
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Db 491 ThrPheLeuValSerThrLeuLeuThrGlnThrPheLeuAlaSerMetGlyLeuVal 510
QY 1594 ATCACTGCTGAGTGGAGTCCCTCGGTAT--TATCTC 1626
Db 511 LeuThrLeuAlaGlyLeuProIleLeuTyrLeuTyrLeu 522

RESULT 10
US-08-825-781-1
; Sequence 1, Application US/08825781
; Patent No. 5843727
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN TUMOR-ASSOCIATED MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,781
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0262 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTUT02
; CLONE: 2236771
; US-08-825-781-1

Alignment Scores:
Pred. No.: 2,09e-46 Length: 245
Score: 524.50 Matches: 102
Percent Similarity: 67.25% Conservative: 52
Best Local Similarity: 44.54% Mismatches: 72
Query Match: 12.73% Indels: 3
DB: 2 Gaps: 2

US-09-667-170a-440 (1-2239) x US-08-825-781-1 (1-245)
QY 1048 ATGCCATTGTCACCATGCTATGCTGACAAAGTGGCTACTTTAGCACCAATTAAT 1107
Db 1 MetProIleValThrIleIleTyrIleLeuThrAsnValAlaTyrThrValLeuAsp 20
QY 1108 GCTGAGGAGTGGCTTTCAAATGAGTGGAGTGCACCTTTCTGAGCGGTACTGGGA 1167
Db 21 MetArgAspIleLeuAlaSerAspAlaValAlaThrPheAlaAspGlnIlePheGly 40
QY 1168 AATTTCTCATTAGCAGTTCGATCTTTGTTGGCCCTCTCTGCTTGGCTCCATGACGGT 1227

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Db 41 IlePheAsnTrpIleLeuProLeuSerValAlaLeuSerCysPheGlyGlyLeuAsnAla 60
QY 1228 GGTGTGTTGCTGTCTCCAGGTTATTCTATGTTGGCTCTCGAGAGGGTCACTTCCAGAA 1287
Db 61 SerIleValAlaAlaSerArgLeuPheValGlySerArgGluGlyHisLeuProAsp 80
QY 1288 ATCCTCTCCATGATTCATGTCGCGACGACACTCTCTACAGCTGTTATTGTTTGGAC 1347
Db 81 AlaIleCysMetIleHisValGluArgPheThrProValProSerLeuLeuPheAsnGly 100
QY 1348 CTTTGACAATGATATGCTCTCTCTGAGACCTCGACAGTCTTTTGAATTTCTCAGT 1407
Db 101 IleMetAlaLeuIleTyrLeuCysValGluAspIlePheGlnLeuIleAsnTyrTrpSer 120
QY 1408 TTTGCCAGGTGGCTTTTATTGGCTGGCAGTGTGGCTGATTTATCTTCGATACAAA 1467
Db 121 PheSerTyrTrpPheValGlyLeuSerIleValGlyGlnLeuTyrLeuArgTrpLys 140
QY 1468 TGCCAGATATGATGCTCTCTTCAAGGTGCCACTGTTTCATCCAGCTTTGTTTCTTC 1527
Db 141 GluProAspArgProArgProLeuLysLeuSerValPhePheProIleValPheCysLeu 160
QY 1528 ACATGCTCTTCAATGCTGCTCTTCCCTCTATTTCGACCCATTTAGTACAGGATGGC 1587
Db 161 CysThrIlePheLeuValAlaValProLeuTyrSerAspThrIleAsnSerLeuIleGly 180
QY 1588 TTCGTCTACATCTGCTGAGTGGAGTCCCTGCTGTTATCTCTTTATT-----ATATGGGAC 1641
Db 181 IleAlaIleAlaLeuSerGlyLeuProPheTyrPheLeuIleIleArgValProGluHis 200
QY 1642 AGAAACCCAGGTGGTTTGAATTAATGTCAGAGAAATAACAGAACATTAATAATAATA 1701
Db 201 LysArgProLeuTyrLeuArgIleValGlySerAlaThrArgTyrLeuGlnValLeu 220
QY 1702 ---CTGGAAGTCTTACCAGAGAGAT 1725
Db 221 CysMetSerValAlaAlaGluMetAsp 229

RESULT 11
US-09-107-532A-4001
; Sequence 4001, Application US/09107532A
; Patent No. 6582275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:

```

230 AlaArgGluMetLysArgProGluLysAspLeuProLysAlaIleLeuGlyLeuSer 249

1054 ATTGTGCACATTGGCTACTGTGTCACAAATGTGGCTACTTTACACACCAATTAAATGCTGAG 1113

250 PheValThrValValTyLeuLeuIleAsnPheValPheLeuLysThrLeuProIleAsp 269

1114 GAGCTGCTGCTTTCAAATGCAGTGCAGTGACCTTTCTGACGGCTACTGGGAAATTC 1173

270 HisLeuAlaGlyAsnLeuAsnAlaAlaSerGluAlaSerAspValIlePheGlyGlyIle 289

1174 --TCATTAGCAGTTCCTGCTTTGCTTGCCTCTCTGCTTTGGTCCATGAACGGTGT 1230

290 GlyGlyLysLeuValThrIleGlyLeuIleSerValTyGlyAlaLeuAsnGlyTy 309

1231 GGTGTTGCTGCTCCAGGTATTCTATCTGTGCTGCTCGAGAGGGTCACCTTCACGAAATC 1290

310 ThrLeuThrGlyIleArgValProTyraMetAlaLeuGluAspLeuProPheSer 329

1291 CTTCTCCATGATTCTGTCGGCAAGCACACTCTCTACACAGCTGTTATTCTTTTGACCCCT 1350

330 LysGlnLeuThrAsnLeuSerLysPheThrValProTyrValProAlaValPheGln 349

1351 TTGCAATG-----ATAATGCTCTCTCTCTGAGACCTCGACAGTCTTTTGAATTCCTC 1404

350 LeuAlaValAlaCysIleMetSerLeuGlySerPheAspPheLeuThrHisMetLeu 369

1405 AGTTTTCACAGTGGCTTTTATTGGCTGGCAGTGTCTGCGCTGATTTATCTTCGTATC 1464

370 IlePheValMetTrpLeuPheThrLeuLeuIleCysIleGlyValSerLeuThrLys 389

1465 AAATCCCATATCATCGTCTCTTCAAGTGCCACTGTC 1506

390 LysAlaProGluLeuProArgProTyrglnValProLeuTy 403

RESULT 12

US-08-132-990A-8

Sequence 8, Application US/08132990A

Patent No. 5834589

GENERAL INFORMATION:

APPLICANT: MERUELO, DANIEL

APPLICANT: YOSHIMOTO, TAKAYUKI

TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/132,990A

FILING DATE: 07-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/084,729

FILING DATE: 29-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/05569

FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/899,075

FILING DATE: 11-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/806,178

FILING DATE: 13-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/627,950

FILING DATE: 14-DEC-1990

## ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 8105-004-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864  
 TELEX: 66441 PENNIE  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 629 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-132-990A-8

## Alignment Scores:

Pred. No.: 4,24e-21 Length: 629  
 Score: 286.00 Matches: 103  
 Percent Similarity: 43.16% Conservative: 80  
 Best Local Similarity: 24.29% Mismatches: 183  
 Query Match: 6.94% Indels: 58  
 DB: 2 Gaps: 12

US-09-667-170A-440 (1-2239) x US-08-132-990A-8 (1-629)

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QY 331 AGAGAGAAAGTGCAGCTGAAGAGAAAGTCACTTTACTGAGGGAGTCTCCATTATCAT 390
Db 23 ArgGluGluThrArgLeuSerArgCysLeuAsnThrPheAspLeuValAlaLeuGlyVal 42
QY 391 GGACCATCATTCAGACGCGAACTTCATCTCTCCCTAAGGGGCTCTCCAGAACACGGGC 450
Db 43 GlySerThrLeuGluAlaGlyValThrValAlaGlyValAlaValaarglu----- 60
QY 451 AGCGTGGGATGCTCTGACATC---TGCAGCGTGTGGGGTCTGCTCACTATTGGA 507
Db 61 AsnAlaGlyProAlaIleValIleSerPheLeuIleAlaAlaSerValLeuAla 80
QY 508 GCTTTGCTTATGCTGAATGGGAACAACATTAAGAAATCTGGAGTCACTACATAT 567
Db 81 GlyLeuCysTyrGlyGluPheGlyAlaArgValProLysThrGlySerAlaTyrLeuTyr 100
QY 568 ATTTTGAAGCTTTTGTGCTCATTACCAAGCTTTTGTACAGTCTGGTGGACTCTCTC 624
Db 101 SerTyrValThrValGlyGluLeuTyrAlaPheIleThrGlyTyrAsnLeuLeuSer 120
QY 625 ---ATAATACGCTCAGCTACTGCT---GTGATATCCCTGGCAATTTGGAGCTACATT 678
Db 121 TyrIleIleGlyThrSerSerValAlaArgAlaTyrPheAlaThrPheAspGluLeu 140
QY 679 CTGGACCATTT-----TTTATTCAA 699
Db 141 GlyArgProIleGlyGluPheSerArgThrHisMetThrLeuAsnAlaProGlyValLeu 160
QY 700 TGTGAATCCCTGCACTTGGCATCAAGCTCAATACAGTCTGGGCATTAAGTGTAGTATG 759
Db 161 AlaGluAsnProAspIlePheAlaValIle-----IleLeuIleLeuThr 176
QY 760 GTCTTAATAGCATGATGTCAGCTGGAGCGCCGGATCCAGATTTCTTAACCTTTTC 819
Db 177 GlyLeuLeuThrLeuGlyValLysGluSerAlaMetValAsnLysIlePheThrCysIle 196
QY 820 AAGCTCAAGCAATCTTGATAATATATAGTCCCTGGAGTTATGCAAGCTAATTAAGTCAA 879
Db 197 AsnValLeuValLeuGlyPheIleMetValSerGly-----PheValLysGlySer 213
QY 880 ACGCAGACCTTTAA----- 894
Db 214 ValLysAsnTyrGlnLeuThrGluGluAspPheGlyAsnThrSerGlyArgLeuCysLeu 233
QY 895 -----GACGCTTTTCAGGAGAGATTCAGATATACGGGGTTGCCACTGGCTTTTAT 948
Db 234 AsnAsnAspThrLysGluGlyLysProGlyValGlyPheMetProPheGlyPheSer 253

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QY 949 TATGGAATG-----TATGCATATGCTGGCTGGTTTACCTCAAC 987
Db 254 GlyValLeuSerClyAlaAlaThrCysPheTyrAlaPheValGlyPheAspCysIleAla 273
QY 988 TTTGTTACTGAAGACTAGAAAACCTGAAACCAATCCCTTGCATATGATATCC 1047
Db 274 ThrThrGlyGluGluValLysAsnProGlnLysAlaIleProValGlyIleValAlaSer 293
QY 1048 ATGCCATTGTCCACCATGCTGCTATGCTGACAAATGTGGCTACTTTACGACCATTAAT 1107
Db 294 LeuLeuIleCysPheIleAlaTyrPhe-----GlyValSerAlaAlaLeuThrLeuMet 311
QY 1108 GCTGAGGAGCTGCTGCTTTCAATGAGTGGCAGTGCACCTTTTCTGAGCGGTACTGGGA 1167
Db 312 MetProTyrPheCysLeuAspAsnAsnSerProArgValIleTyrAlaMetAlaGluAspGly 331
QY 1168 -----AATTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTTGGC 1215
Db 332 TrpGluGlyAlaLysTyrAlaValAlaValGlySerLeuCysAlaLeuSer-----Ala 349
QY 1216 TCCATGAACGGTGTGTTGCTGCTCCAGGTATTCTATGTTTGGCTCTCGAGAGGT 1275
Db 350 SerLeuLeuGlySerMetPheProMetProArgValIleTyrAlaMetAlaGluAspGly 369
QY 1276 CACTTCCAGAAATCCTCTCCATGATTCAATGTCGCGAAGCACACTCTCTACAGCTGTT 1335
Db 370 LeuLeuPheLysPheLeuAlaAsnValAsnAspArgThrLysThrProIleAlaThr 389
QY 1336 ATTGTTTTCACCTTTGACAAATGATAATGCTCTTCTCTGGAGACCTCCAGACTCTTTTG 1395
Db 390 LeuAlaSerGlyAlaValAlaAlaValMetAlaPheLeuPheAspLeuLysAspLeuVal 409
QY 1396 AATTCTCAGTTTTCAGCTGGCTGCTTTTATTTGCGCTGGCAGTCTGGCTGATTTAT 1455
Db 410 AspLeuMetSerIleGlyThrLeuLeuAlaTyrSerLeuValAlaAlaCysValLeuVal 429
QY 1456 CTTGATACAAA 1467
Db 430 LeuArgTyrGln 433

RESULT 13
PCT-US92-09382-8
; Sequence 8, Application PC/TUS9209382
; GENERAL INFORMATION:
; APPLICANT: MERUELO, DANIEL
; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09382
; FILING DATE: 19921213
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Livnat, Shmuel
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: MERUELO=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 628-5197
; INFORMATION FOR SEQ ID NO: 8:

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; SEQUENCE CHARACTERISTICS:  
; LENGTH: 629 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US92-09382-8

## Alignment Scores:

Pred. No.: 4,24e-21 Length: 629  
Score: 286.00 Matches: 103  
Percent Similarity: 43.16% Conservative: 80  
Best Local Similarity: 24.29% Mismatches: 183  
Query Match: 6.94% Indels: 58  
DB: 5 Gaps: 12

US-09-667-170A-440 (1-2239) x PCT-US92-09382-8 (1-629)

```
QY 331 AGAGAGAAAGTGCAGCTGAAGAGAAAGTCACTTTACTGAGGGAGTCTCCATATATCAT 390
D 23 ArgGluGluThrArgLeuSerArgCysLeuAsnThrPheAspLeuValAlaLeuGlyVal 42
QY 391 GGCACCATCATGAGGAGGAAATCTTCATCTCTCTTAAGGGCGTCTCCGAACACGGGC 450
D 43 GlySerThrLeuGlyAlaGlyValThrValLeuAlaGlyAlaValAlaArgGlu----- 60
QY 451 AGCGTGGGCATCTCTCTGACCATC---TGGAGGGTGTGGGGTCTCTCTACTATTGGA 507
D 61 AsnAlaGlyProAlaIleValIleSerPheLeuIleAlaIleAlaLeuAlaSerValLeuAla 80
QY 508 GCTTTGTCTTATGCTGAATTTGGAAACAACATAAAGAAATCTGGAGGTCAATPACACATAT 567
D 81 GlyLeuCysTyrGlyGluPheGlyAlaArgValProLysThrGlySerAlaTyrLeuTyr 100
QY 568 ATTTGGAGCTTTGGTCCATACAGCTTTTGTACGAGTGTGGTGGAACTCTC--- 624
D 101 SerTyrValThrValGlyGluLeuTrpAlaPheIleThrGlyTrpAsnLeuIleLeuSer 120
QY 625 ---ATAAGCGCTGCAGTACTGCT---GTGATATCCTCGCATTTGGAGCTACATAT 678
D 121 TyrIleIleGlyThrSerSerValAlaArgAlaTrpSerAlaThrPheAspLeuIle 140
QY 679 CTGGAACCATTT-----TTTATCAA 699
D 141 GlyArgProIleGlyGluPheSerArgThrHisMetThrLeuAsnAlaProGlyValLeu 160
QY 700 TGTGAATCCCTGAACCTCCGATCAAGCTCATACAGCTGTGGGATACTAGTAGTG 759
D 161 AlaGluAsnProAspIlePheAlaValIleIle-----IleLeuIleLeuThr 176
QY 760 GTCCTAAATAGCATAGTGTGAGTGGAGCGCGGATCCAGATTTCCTTAACCTTTTGC 819
D 177 GlyLeuThrLeuGlyValLysGluSerAlaMetValAsnLysIlePheThrCysIle 196
QY 820 AAGCTCACAGCAATCTGATAATTATAGTCCCTGGAGTTATGCAAGTAATTAAGTCAA 879
D 197 AsnValLeuValLeuGlyPheIleMetValSerGly-----PheValLysGlySer 213
QY 880 AGCGAAGCTTTAA----- 894
D 214 ValLysAsnTrpGlnLeuThrGluGluAspPheGlyAsnThrSerGlyArgLeuCysLeu 233
QY 895 -----GAGCCCTTTTCAGGAAGAGATTCAAGTATTACGGGTTCGACCTGGCTTTTAT 948
D 234 AsnAsnAspThrLysGluGlyLysProGlyValGlyGlyPheMetProPheGlyPheSer 253
QY 949 TATGGAATG-----TATGCATATGCTGGCTGGTTTTACCTCAAC 987
D 254 GlyValLeuSerGlyAlaAlaThrCysPheTyrAlaPheValGlyPheAspCysIleAla 273
QY 988 TTTGTACTGAAGAGTAGAAACCCCTGAAAAACCATCCCTTCCCTTGCATATATATATCC 1047
D 274 ThrThrGlyGluGluValLysAsnProGlnLysAlaIleProValGlyIleValAlaSer 293
```

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QY 1048 ATGCCCATTTGTACCATTTGCTGTATGCTGACAAATGTGGCCTACTTTAGACATTAAT 1107
D 294 LeuLeuIleCysPheIleAlaTyrPhe-----GlyValSerAlaAlaLeuThrLeuMet 311
QY 1108 GCTGAGGAGCTGTGCTTTCAATGAGTGGAGTGGAGCTTTTCTTGAGCGGCTACTGGGA 1167
D 312 MetProTyrPheCysLeuAspAsnSerProLeuProAspAlaPheLysHisValGly 331
QY 1168 -----AATTCTCATAGCAGTCCGATCTTTTGTGCTCTCTCTGCTTTGGC 1215
D 332 TrpGluGlyAlaLysTyrAlaValAlaValGlySerLeuCysAlaLeuSer-----Ala 349
QY 1216 TCCATGAACGGTGTGTTGCTGTCTCCAGTTATCTATGTTGCTGTCGAGAGGCT 1275
D 350 SerLeuLeuGlySerMetPheProMetProArgValIleTyrAlaMetAlaGluAspGly 369
QY 1276 CACCTTCCAAAATCTCTCCATGATTCATGTCGGCAGCACACTCTCTACACAGCTTT 1335
D 370 LeuLeuPheLysPheLeuAlaAsnValAsnAspArgThrLysThrProIleAlaThr 389
QY 1336 ATTGTTTTGCACCTTTGACAATGATAATGCTCTCTCGAGACCTCGACAGCTTTTG 1395
D 390 LeuAlaSerGlyAlaValAlaAlaValMetAlaPheLeuPheAspLeuLysAspLeuVal 409
QY 1396 AATTCTCAGTTTGGCAGTGGCTTTTATTGGGCTGGCAGTTGCTGGGCTGATTTAT 1455
D 410 AspLeuMetSerIleGlyThrLeuLeuAlaTyrSerLeuValAlaAlaCysValLeuVal 429
QY 1456 CTTTCGATACAAA 1467
D 430 LeuArgTyrGln 433
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## RESULT 14.

US-09-134-001C-4290  
; Sequence 4290, Application US/09134001C  
; Patent No. 6380370

## GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4290  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4290

## Alignment Scores:

Pred. No.: 8,97e-21 Length: 521  
Score: 282.50 Matches: 135  
Percent Similarity: 43.39% Conservative: 108  
Best Local Similarity: 24.11% Mismatches: 206  
Query Match: 6.86% Indels: 111  
DB: 4 Gaps: 26

US-09-667-170A-440 (1-2239) x US-09-134-001C-4290 (1-521)

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QY 127 TTTTAT---CATATCTCGATTTTGGATTCTTTTGTCTCATCTACTGATTACGGA 183
D 8 PheTyrLeuHisValAspPheLeuIleArgIleValLysGluCysLeuLeuThr--- 26
QY 184 AAGCCTGTGTCTCCACCATCTCCAAAGAGAGGTGTACTCGAGGAAATTTAACGGGAGG 243
D 27 ---HisValAsnSerLysLeuMetLeuTrpArgPheValMetGlySerPheAsnArg 45
QY 244 CTGCCTTCCCTGGGCAACAGGAGCCACCTGGGCGAGCGCTTTTTCAGAAAGACGCC 303
```

Db 46 MetThr-----ArglysluAsnPro-----Thrile 54  
QY 304 TTTTCAGGAAGAGCGCTTTTCAGGAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACT 363  
Db 55 TyrGlnSerLysAspGly-----HisLeuLysArgThrLeuArg 67  
QY 364 TTACTGAGGAGGAGTCTCCATTATCATATGACCATTCATTGGCAGCAGGAATCTTCATCTCT 423  
Db 68 ValArgAspPheLeuAlaLeuGlyValGlyThrIleValSerThrSerIlePheThrLeu 87  
QY 424 CTAAGGGGCTCTCCAGAACCGGCGAGCGTGGGCATGCTCTGACCATCTGAGCGGTG 483  
Db 88 ProGlyValValAlaAlaGluHisAlaGlyProAlaValSerLeuSer-----PheLeuLeu 106  
QY 484 TGTGGGGCTCTCACTATTTGGAGCTTTGTCTATGCTGTAATTCGGGACCAACTATAAG 543  
Db 107 AlaAlaIleValAlaGlyLeuValAlaPheThrIleAlaGluMetAlaSerThrMetPro 126  
QY 544 AAATCTGGAGGTCAATACACATATATTTTGGAGTCTTTGGTCCATTACCACTTTTCTA 603  
Db 127 PheAlaGlySerAlaTyr-SerTrpIleAsnValLeuPheGlyGluLeuPheGlyTrpVal 146  
QY 604 CGAGTCTGGTGGAACTCTCATATACGCCCTGCAGCTACTGCTGATATCCCTGCACA 663  
Db 147 AlaGlyTrpAla---LeuLeuAlaGluTyrPheIleAlaValAlaPheValAlaSerGly 165  
QY 664 TTTTGA-----CGCTACATTTCTGGAACCATTTTATTCATATGTAATCCCTGAA 714  
Db 166 PheSerAlaAsnLeuArgGlyLeuIleAlaProLeuGlyIle-----SerLeuProLys 183  
QY 715 CTT-----GGCATCAAGTCACTTACAGCTGTGGGC 744  
Db 184 SerLeuSerAsnProPheGlySerAsnGlyGlyValIleAspIleIleAlaValVal 203  
QY 745 ATAAGTGTAGTATGGTCTTAATACCATGAGTGTGAGCGCGCGGATCCAGATT 804  
Db 204 IleIleLeuThrAlaLeuLeuLeuSerArgGlyMetAsnGluAlaAlaArgMetGluAsn 223  
QY 805 TTTCTAACTTTTGAAGTCCACAGCAATTCGATAATATTATAGTCCCTGGAGTTATGCAG 864  
Db 224 ValLeuValIleLeuLysValLeuAlaIleIleLeuPheValIleValGlyLeuThrAla 243  
QY 865 CTAATTAAGGTCAAAACCGCAGAACTTTAAAGAC----- 897  
Db 244 Ile-----AsnPheSerAsnTyrIleProPheIleProGluHisLys 257  
QY 898 -----GCCCTTTTCAGGAGAGATTCAAGTATTACGGGTTCGCCAGTGGCT 942  
Db 258 ValThrGluThrGlyAspPheGlyGly----- 266  
QY 943 TTTTATTATGGAATGTATGATATGCTGGCTGGTGTTCCTCAACTTGTGT----- 993  
Db 267 ---TrpGlnGlyIleTyrAlaGlyValSerMetIlePheLeuAlaTyrIleGlyPheAsp 285  
QY 994 -----ACTGAGAAGTAGAAGAAACCCCTGAAACACATTCCTCCCTTCGAATA 1038  
Db 286 SerIleAlaAlaAsnSerAlaGluAlaIleAsnProGlnLysThrMetProArgGlyIle 305  
QY 1039 TGTATATCATCCGCAAT-----GTCCACCATGGCTGTGCTGTGCACAAAT 1083  
Db 306 LeuGlySerLeuIleValAlaIleValLeuPheValAlaValAlaValLeuValGly 325  
QY 1084 GTGGCTACTTTACGACCATTAATGTGTGAGAGCTGCTCTTTCAAATGACGTGGCGATG 1143  
Db 326 MetPheHisTyrSerGln-----TyrAlaAspAsnAlaGluProVal 339  
QY 1144 ACCTTTTCTGAGCGGTACTGGAAATTTCTCATAGCA-----GTTCCGATCTTTGTT 1197  
Db 340 GlyTrpAlaLeuArgGluSerGlyHisGlyIleIleAlaAlaIleValGlnAlaIleSer 359  
QY 1198 GCCTCTCTCTGCTTGGCTCCATGAACGTTGGTGTGTGCTCTCCAGGTTATCTAT 1257

Db 360 ValIleGlyMetPheThrAlaLeuIleGlyMetMetLeuAlaGlySerArgLeuLeuTyr 379  
QY 1258 GTTGGCTCTCAGAGGTCACCTTTCAGAAATCTCTCCATGATTCATGTCGCGAAGCAC 1317  
Db 380 SerPheGlyArgAspGlyLeuLeuProSerTrpLeuSerGlnLeuAsn---HisLysHis 398  
QY 1318 ACTCCTCTACAGCTGTATTGTTTGCACCTTTGACATGATGATGCTCTCTCTGGA 1377  
Db 399 LeuProAsnArgAlaLeuAlaIle-----LeuThrIleIleGlyValIleGly 415  
QY 1378 GAC-----CTCGACAGCTTTTGAATTCCTCAGCTTTTGCAGGTGG 1419  
Db 416 SerMetPheProPheAlaPheLeuAlaGlnLeuIleSerAlaGlyThrLeuValAlaPhe 435  
QY 1420 CTTTATTATGGCTGGCAGTTGTGGCTGATTTATCTTCGATACAAATGCCCATATG 1479  
Db 436 MetPheValSerLeuAlaMetTyrArgLeu-----ArgLysArgGluGlyLysAspLeu 453  
QY 1480 CATGCTCTCT---TTCAAGTGGCAGCTGTTCT-----ATCCAGCTTTGTTTCTCTCACA 1530  
Db 454 ProLysProGluPheLysLeuProLeuTyrProIleLeuProAlaIle---ThrPheIle 472  
QY 1531 TGCTCTCTCATGTTGCTCCCTTCCCTC---TATTGGACCCCACTTACTACAGGATGGC 1587  
Db 473 LeuValLeuLeuValPheTrpGlyLeuSerPheGluAlaLysLeuTyrThrLeuIleTrp 492  
QY 1588 TTCTCATCTCTGACTGAGTCCCTGCGTATTCATCTTTATTTATATATGACACAGAA 1647  
Db 493 PheIleVal-----GlyIleIleIleTyrLeuIleTyrGlyIleArgHisSerLys 509

## RESULT 15

US-08-132-990A-4  
; Sequence 4, Application US/08132990A  
; Patent No. 5834589  
; GENERAL INFORMATION:  
; APPLICANT: MERUELO, DANIEL  
; APPLICANT: YOSHIMOTO, TAKAYUKI  
; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/132,990A  
; FILING DATE: 07-OCT-1993  
; PRIORITY DATA:  
; APPLICATION NUMBER: 08/084,729  
; FILING DATE: 29-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/05569  
; FILING DATE: 11-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/899,075  
; FILING DATE: 11-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/806,178  
; FILING DATE: 13-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/627,950  
; FILING DATE: 14-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 8105-004-999

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864  
 TELEX: 66441 PENNIE  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 622 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-132-990A-4

Alignment Scores:  
 Pred. No.: 2,03e-20 Length: 622  
 Score: 279.50 Matches: 102  
 Percent Similarity: 42.82% Conservations: 80  
 Best Local Similarity: 24.00% Mismatches: 176  
 Query Match: 6.78% Indels: 67  
 Gaps: 13

US-09-667-170A-440 (1-2239) x US-08-132-990A-4 (1-622)

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Oy 331 AGAGAGAAAGTCAGCTCAAGAGGAAAGTCACCTTTACTGAGGGAGTCTCCATTATCAT 390
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Db 23  ArgGluGluSerArgLeuSerArgCysLeuAsnThrTyrAspLeuValAlaLeuGlyVal 42
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 391 GGCACCATCATGAGCAGGAAATCTTACTCTCTAAGGGGGTCTCCAGAACAGGGGC 450
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 43  GlySerThrLeuGlyAlaGlyValTyrValLeuAlaGlyAlaValAlaArgGlu----- 60
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 451 AGCGTGGGCATCTCTCAGCATC--TGGACGGGTGTGGGGTCTCTCATTATTGGA 507
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 61  AsnAlaGlyProAlaIleValIleSerPheLeuIleAlaLeuAlaSerValLeuAla 80
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 508 GOTTGTCTTATGCTGAATGGAACAACATAAAGAAATCTGGAGGTCATTACACATAT 567
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 81  GlyLeuCysTyrGlyGluPheGlyAlaArgValProLysThrGlySerAlaTyrLeuTyr 100
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 568 ATTTGGGAAGCTTTGGTCCATTACAGCTTTTGTACGAGTCTGGTGGGAACTCTC--- 624
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 101 SerTyrValThrValGlyGluLeuTrpAlaPheIleThrGlyTrpAsnLeuIleLeuSer 120
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 625 ---ATAATACGCTGAGTCTACTCT---GTGATATCCCTGGCATTGAGGCTACATT 678
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 121 TyrIleIleGlyThrSerSerValAlaArgAlaTrpSerAlaThrPheAspGluLeuIle 140
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 679 CTGGAACCATTT-----TTTATTCAA 699
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 141 GlyLysProIleGlyGluPheSerArgGlnHisMetAlaLeuAsnAlaProGlyValLeu 160
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 700 TGTGAATCCCTGAACCTCGCATCAAGCTCATACAGCTGTGGGCATACTAGTGATG 759
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 161 AlaGlnThrProAspIlePheAlaValIleIle-----IleIleIleLeuThr 176
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 760 GTCTAAATAGCATGAGTCTAGCTGAGCGCCGGATCCAGATTTCTTAACCTTTTGC 819
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 177 GlyLeuThrLeuGlyValLysGluSerAlaMetValAsnLysIlePheThrCysIle 196
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 820 AAGCTCACAGCAATCTGATAATTATAGTCCCTGGAGTTATGACGCTAANTAAAGTCAA 879
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 197 AsnValLeuValLeuCysPheIleValValSerGly-----PheValLysGlySer 213
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 880 AGCAGAACTTTAAAGACGCTTTTCCAGGAAGAGATTCAAGTATTACGGGGTGGCAGTC 939
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 214 IleLysAsnTrpGln-----LeuThrGluLysAsnPheSerCysAsnAsnAspThr 231
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 940 GCTTTTATTATGGA----- 954
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 232 AsnValLysTyrGlyGluGlyGlyPheMetProPheGlyPheSerGlyValLeuSerGly 251
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 955 -----ATGATGCATATGCTGGCTGTTTACCTCAACTTTGTACTGAAGAA 1002
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```

```

Db 252 AlaAlaThrCysPheTyrAlaPheValGlyPheAspCysIleAlaThrThrGlyGluGlu 271
Oy 1003 GTAGAAAACCTGAAAAACCATTCCTCCCTTGCAATATGTATATCCATGCCATTGTCCACC 1062
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 272 ValLysAsnProGlnLysAlaIleProValGlyIleValAlaSerLeuLeuIleCysPhe 291
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 1063 ATTGGCTATGTGTGCACAAATGTGGCCTACTTTACGACCACTTAATGTGTGAGGAGCTGCTG 1122
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 292 Ile-----AlaTyrPhe---GlyValSerAlaAlaLeuThrLeu 303
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 1123 CTTTCAAATCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGAAATTTC----- 1173
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 304 MetMetProTyrPheCysLeuAspIleAspSerProLeuProGlyAlaPheLysHisGln 323
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 1174 -----TCATTAGCAGTTCGGATCTTTGTGGCCCTCTCTGCTGCTTT 1212
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 324 GlyTrpGluGluAlaLysTyrAlaValAlaIleGlySerLeuCysAlaLeuSerThr--- 342
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 1213 GGCTCCCATGAACGGTGTGTGTCTCTCCAGGTTATTCTATGTGTGGTCTCGAGAG 1272
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 343 ---SerLeuLeuGlySerMetPheProMetProArgValIleTyrAlaMetAlaGluAsp 361
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 1273 GGTCACTTCCAGAAATCTCTCCATCATTCATGTCGCGAAGCACACTCTCTACCACT 1332
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 362 GlyLeuLeuPheLysPheLeuAlaLysIleAsnAsnArgThrLysThrProValIleAla 381
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 1333 GTTATTCTTTCACCCCTTTGACAATGATAATGCTCTCTCGAGACCTCGACAGTCTT 1392
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 382 ThrValThrSerGlyAlaIleAlaValMetAlaPheLeuPheGluLeuLysAspLeu 401
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 1393 TTGAATTTCTCAGTTTTCAGGCTGGCTTTTATGGCTGGCAGTGTGTGGGCTGATT 1452
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 402 ValAspLeuMetSerIleGlyThrLeuLeuAlaTyrSerLeuValAlaAlaCysValLeu 421
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Oy 1453 TATCTTCATACAAA 1467
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 422 ValLeuArgTyrGln 426
    |||||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```

Search completed: October 31, 2003, 11:07:49  
 Job time : 64.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 31, 2003, 11:02:11 ; Search time 200 Seconds

(without alignments)  
3831.960 Million cell updates/sec

Title: US-09-667-170A-440

Perfect score: 4120

Sequence: 1 g9aggttgagtgagcagag.....ttattaaaaaaaaaaaaa 2239

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 642050 segs, 171146064 residues

Total number of hits satisfying chosen parameters: 1284100

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODBL=frame+ n2p.model -DEV=xlp  
-O=/cgn2\_1/USPTO.spool/US09667170/runat\_31102003\_104953\_10440/app.query.fasta\_1.2375  
-DB=Published Applications AA -OPMT=fastan -SUFFIX=xapb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNIT8=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09667170 @CGN 1.1\_141 @runat\_31102003\_104953\_10440  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOC=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /cgn2\_6/prodata/1/pubpaa/FCI\_NEW\_PUB.pcp.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pcp.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pcp.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pcp.\*
- 6: /cgn2\_6/prodata/1/pubpaa/FCI\_NEW\_PUB.pcp.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pcp.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pcp.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US09A\_PUBCOMB.pcp.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pcp.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pcp.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US09D\_NEW\_PUB.pcp.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*
- 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pcp.\*
- 16: /cgn2\_6/prodata/1/pubpaa/US10D\_NEW\_PUB.pcp.\*
- 17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pcp.\*
- 18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	2519	61.1	501	15	US-10-163-866-48	Sequence 48, Appl
2	2519	61.1	501	15	US-10-163-866-49	Sequence 49, Appl
3	2298	55.8	502	12	US-10-214-867A-13	Sequence 13, Appl
4	1210.5	29.4	507	15	US-10-163-866-54	Sequence 54, Appl
5	1206.5	29.3	524	15	US-10-163-866-37	Sequence 37, Appl
6	1198.5	29.1	507	15	US-10-163-866-38	Sequence 38, Appl
7	1198.5	29.1	507	15	US-10-163-866-39	Sequence 39, Appl
8	1198	29.1	512	12	US-10-214-867A-10	Sequence 10, Appl
9	1156.5	28.1	515	12	US-10-214-867A-12	Sequence 12, Appl
10	1156.5	28.1	515	15	US-10-163-866-40	Sequence 40, Appl
11	1131.5	27.5	511	15	US-10-163-866-41	Sequence 41, Appl
12	1131.5	27.5	511	15	US-10-163-866-42	Sequence 42, Appl
13	1111.5	27.0	511	12	US-10-214-867A-11	Sequence 11, Appl
14	1101.5	26.7	535	15	US-10-163-866-43	Sequence 43, Appl
15	1101.5	26.7	535	15	US-10-163-866-44	Sequence 44, Appl
16	1097	26.6	533	12	US-10-214-867A-9	Sequence 9, Appl
17	1075.5	26.1	487	15	US-10-163-866-46	Sequence 46, Appl
18	1067.5	25.9	487	15	US-10-163-866-45	Sequence 45, Appl
19	1051.5	25.5	530	12	US-10-214-867A-1	Sequence 1, Appl
20	1048	25.4	517	10	US-09-815-923-16	Sequence 16, Appl
21	1039	25.2	523	12	US-10-214-867A-4	Sequence 4, Appl
22	1039	25.2	523	15	US-10-163-866-47	Sequence 47, Appl
23	732	17.8	414	9	US-09-925-297-747	Sequence 747, Appl
24	513	12.5	97	10	US-09-738-973-586	Sequence 586, Appl
25	513	12.5	97	10	US-09-854-133-586	Sequence 586, Appl
26	513	12.5	97	15	US-10-144-649A-586	Sequence 586, Appl
27	513	12.5	114	15	US-10-144-649A-742	Sequence 742, Appl
28	412.5	10.0	180	15	US-10-163-866-50	Sequence 50, Appl
29	406.5	9.9	179	9	US-09-864-761-43216	Sequence 43216, A
30	401	9.7	166	12	US-10-029-386-32531	Sequence 32531, A
31	351	8.5	507	15	US-10-156-761-9780	Sequence 9780, Ap
32	327.5	7.9	492	15	US-10-156-761-14414	Sequence 14414, A
33	323	7.8	462	12	US-10-287-274-345	Sequence 345, App
34	322	7.8	456	9	US-09-815-242-4932	Sequence 4932, Ap
35	322	7.8	463	9	US-09-815-242-10662	Sequence 10662, A
36	303.5	7.4	472	15	US-10-156-761-14823	Sequence 14823, A
37	303.5	7.4	480	15	US-10-156-761-9855	Sequence 9855, Ap
38	295	7.2	619	12	US-09-741-153-4	Sequence 4, Appl
39	295	7.2	619	12	US-10-353-958-4	Sequence 4, Appl
40	286.5	7.0	619	12	US-09-741-153-2	Sequence 2, Appl
41	286.5	7.0	619	12	US-10-353-958-2	Sequence 2, Appl
42	286	6.9	629	15	US-10-157-031-34	Sequence 34, Appl
43	262	6.4	470	9	US-09-815-242-12078	Sequence 12078, A
44	257.5	6.2	482	9	US-09-815-242-12941	Sequence 12941, A
45	255.5	6.2	489	15	US-10-156-761-8760	Sequence 8760, Ap

ALIGNMENTS

RESULT 1

US-10-163-866-48  
; Sequence 48, Application US/10163866  
; Publication No. US20030027188A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-080C  
; CURRENT APPLICATION NUMBER: US/10163,866  
; PRIOR FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/338,733  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/357,600  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48  
; LENGTH: 501



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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-48

Alignment Scores:
  2.41e-228      Length: 501
Pred. No.:      2519.00    Matches: 498
Score:          96.51%    Conservative: 0
Percent Similarity: 96.51% Mismatches: 0
Best Local Similarity: 61.14% Indels: 18
Query Match:      15      Gaps: 1
DB:

US-09-667-170A-440 (1-2239) x US-10-163-866-48 (1-501)

QY 184 AAGCCTGTGTGTCACCATCTCCAAAGAGAGGTACCTGCAGGGAAATGTTAAACGGGAGG 243
Db 4 LysProValValSerThrIleSerLysGlyTyrLeuGlnGlyAsnValAsnGlyArg 23
QY 244 CTGCTTCTCCGGGCAACAGAGAGCCACTGGGAGGAGCGCTTTCAGGAAGAGACGCC 303
Db 24 LeuProSerLeuGlyAsnLysGluProGlyGln----- 35
QY 304 TTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTCAGCTCAAGAGAAAGTCACT 363
Db 36 -----GluLysValGlnLeuLysArgLysValThr 45
QY 364 TPACTGAGGGAGTCTCCATTATCATATGCGACCATCATTTGGAGCAGGAATCTTCATCTCT 423
Db 46 LeuLeuArgGlyValSerIleIleGlyThrIleIleGlyAlaGlyIlePheIleSer 65
QY 424 CCTAAGGGCGCTCCAGACAGCGGACGCGGCGATGCTCTCAGCACCCTGCGAGCGTG 483
Db 66 ProLysGlyValLeuGlnAsnThrGlySerValGlyMetSerLeuThrIleTrpThrVal 85
QY 484 TGTGGGTCTCTCACTATTTGGAGCTTGTCTATGCTGTAATGGGAACAACTATAAG 543
Db 86 CysGlyValLeuSerLeuPheGlyAlaLeuSerTyrAlaGluLeuGlyThrThrIleLys 105
QY 544 AAATCGAGGTCATACACATATATTTTGAAGTCTTTGGTCCATTACCGCTTTTGTGA 603
Db 106 LysSerGlyGlyHisTyrThrTyrIleLeuGluValPheGlyProLeuProAlaPheVal 125
QY 604 CGAGTCTGGTGAAGTCTCTATATAGCCCTGCGAGTCTGCTGATATCCCTGGCA 663
Db 126 ArgValTrpValGluLeuLeuIleArgProAlaAlaThrAlaValIleSerLeuAla 145
QY 664 TTTGACGCTACATCTGGAACCATTTTATTCATATGTAATCCCTGAATTCGATC 723
Db 146 PheGlyArgTyrIleLeuGluProPhePheIleGlnCysGluIleProGluLeuAlaIle 165
QY 724 AAGCTCATACAGCTGTGGGCATACTGTAGTATGCTGCTTAATAAGCATGATGTCAGC 783
Db 166 LysLeuIleThrAlaValGlyIleThrValValMetValLeuAsnSerMetSerValSer 185
QY 784 TGGAGCGCCGGATCCAGATTTTCTTAACCTTTTGAAGTCAACAGCAATCTGATAAT 843
Db 186 TrpSerAlaArgIleGlnIlePheLeuThrPheCysLysLeuThrAlaIleLeuIle 205
QY 844 ATAGTCCCTGGAGTTATGAGCTAATTAAGTCAACAGCAATCTTAAGACGCCCTTT 903
Db 206 IleValProGlyValMetGlnLeuIleLysGlyGlnThrGlnAsnPhelysAspAlaPhe 225
QY 904 TCAGGAAGATCAAGTATACGGGTGGCGCTGCTTTTATATGGAATGATGCA 963
Db 226 SerGlyArgAspSerSerIleThrArgLeuProLeuAlaPheTyrGlyMetTyrAla 245
QY 964 TATGCTGGCTGTTTACCTCACTTTGTTACTGGAAGAGTAGAAAACCTGAAAAACC 1023
Db 246 TyrAlaGlyTrpPheTyrLeuAsnPheValThrGluGluValGluAsnProGluLysThr 265
QY 1024 ATTCCCTTGCAATATGTATATCCATGGCCATTTGTCACCATTTGGCTATGCTGACAAAT 1083
Db 266 IleProLeuAlaIleCysIleSerMetAlaIleValThrIleGlyTyrValLeuThrAsn 285

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QY 1084 GTGCGCTACTTTACGACCAATTAATGCTGAGAGCTGCTGCTTTCAATGACAGTGGCAGTG 1143
Db 286 ValAlaTyrPheThrThrIleAsnAlaGluLeuLeuSerAsnAlaValAlaVal 305
QY 1144 ACCTTTCTGAGCGGCTACTGGGAATTTCTCATTAGCAGTTCGGATCTTTGTTCGCTC 1203
Db 306 ThrPheSerGluArgLeuLeuGlyAsnPheSerLeuAlaValProIlePheValAlaLeu 325
QY 1204 TCCTGCTTTGGCTCCATGAACGGTGGTGTGTTGCTGCTCCAGGTTATTTCTATGTTGCG 1263
Db 326 SerCysPheGlySerMetAsnGlyGlyValPheAlaValSerArgLeuPheTyrValAla 345
QY 1264 TCTCAGAGGGTCACCTTCAGAAATCCTCTCCATGATTCAATGTCGCAAGACACATCCT 1323
Db 346 SerArgGluGlyHisLeuProGluIleLeuSerMetIleHisValArgLysHisThrPro 365
QY 1324 CTACCACTGCTTATGTTTTCACCTTTCACCAATGATATGCTCTTCTCTGGAGACCTC 1383
Db 366 LeuProAlaValIleValLeuHisProLeuThrMetIleMetLeuPheSerGlyAspLeu 385
QY 1384 GACAGTCTTTTGAATTTCCCTCAGTTTTCAGGTTGGCTTTTATTTGGGCTGGCAGTTGCT 1443
Db 386 AspSerLeuLeuAsnPheLeuSerPheAlaArgTrpLeuPheIleGlyLeuAlaValAla 405
QY 1444 GGGCTGATTTATCTTCGATACAAATGCCAGATATGATGCTGCTTCAAGGTGCCACTG 1503
Db 406 GlyLeuIleTyrLeuArgTyrLysCysProAspMetHisArgProPheLysValProLeu 425
QY 1504 TTCATCCAGCTTGTGTTTCTTCACATGCTCTTCATGTTGCTTCTTCTCTTATTTCG 1563
Db 426 PheIleProAlaLeuPheSerPheThrCysLeuPheMetValAlaLeuSerLeuTyrSer 445
QY 1564 GACCATTTAGTACAGGATTCCTCTCATCATCTCTGAGTGGAGTCCCTGCGTATTAT 1623
Db 446 AspProPheSerThrGlyIleGlyPheValIleThrLeuThrGlyValProAlaTyrTyr 465
QY 1624 CTCTTTATATATGGCAAGAACCCAGGTGGTTTGAATAATGTCAGAAATAAC 1683
Db 466 LeuPheIleIleTrpAspLysLysProArgTrpPheArgIleMetSerGluLysIleThr 485
QY 1684 AGAATTTACAAATAATCTGGAAGTTGTACCAAGAAAGATAAGTTA 1731
Db 486 ArgThrLeuGlnIleIleLeuGluValValProGluLysAspLysLeu 501

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## RESULT 2

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US-10-163-866-49
; Sequence 49, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLIC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-49

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## Alignment Scores:

Pred. No.: 2,41e-228 Length: 501  
Score: 2519.00 Matches: 498  
Percent Similarity: 96.51% Conservative: 0  
Best Local Similarity: 96.51% Mismatches: 0  
Query Match: 61.14% Indels: 18  
DB: 15 Gaps: 1

US-09-667-170A-440 (1-2339) x US-10-163-866-49 (1-501)

QY	184	AAGCCTCTGTGTCACCATCTCCAAAGAGAGGTTCCTGCAGGAAATGTTAAACGGAGG	243
DB	4	LysProValValSerThrIleSerLysGlyGlyTyrLeuGlnGlyAsnValAsnGlyArg	23
QY	244	CTGCCCTCCCTGGGCAACAGAGCCACCTGGGAGAGCCCTTTTCAGNAGAGAGCC	303
DB	24	LeuProSerLeuGlyAsnLysGluProProGlyGln	35
QY	304	TTTTTCAGAGAGAGAGCCCTTTTCAGAGAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACT	363
DB	36	-----GluysValGlnLeuLysArgLysValThr	45
QY	364	TTACTAGGGGAGRTCCATTATCATTTGCGACCATCATTTGGAGCAGGAATCTTCATCTCT	423
DB	46	LeuLeuArgGlyValSerIleIleIleGlyThrIleIleGlyAlaGlyIlePheIleSer	65
QY	424	CCTAAGGCGTCTCCAGAACACGGGACCTGGGCGATGCTCTGACCATCTGGACGGTG	483
DB	66	ProLysGlyValLeuGlnAsnThrGlySerValGlyMetSerLeuThrIleThrVal	85
QY	484	TGTGGGTCCTCTCACTATTTTGGAGCTTGCTTATGCTGAATGGGAACCACTATAAG	543
DB	86	CysGlyValLeuSerLeuPheGlyAlaLeuSerTyrAlaGluLeuGlyThrIleLys	105
QY	544	AAATCTGAGGTCAATACACATATTTTGAAGTCTTTTGGTCCATACACAGCTTTTGTGA	603
DB	106	LysSerGlyGlyHisTyrThrTyrIleLeuGluValPheGlyProLeuProAlaPheVal	125
QY	604	CGAGTCTGGTGGBACTCCTATATACGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA	663
DB	126	ArgValTrpValGluLeuLeuIleIleArgProAlaAlaThrAlaValIleSerLeuAla	145
QY	664	TTTGACCTCATCTCTGGAACCACTTTTATTCATGTGAATCCCTGGAATCTGCGATC	723
DB	146	PheGlyArgTyrIleLeuGluProPheIleGlnCysGluIleProGluLeuAlaIle	165
QY	724	AAGTCAATACAGCTGTGGGCAACTAGTGTGATGTCCTTAATATGATGATGATGATG	783
DB	166	LysLeuIleThrAlaValGlyIleThrValValMetValLeuAsnSerMetSerValSer	185
QY	784	TGGAGCGCCCGATCCAGATTTTCTTAACCTTTTGCAGCTCACAGCAATCTGATATT	843
DB	186	TrpSerAlaArgIleGlnIlePheLeuThrPheCysLysLeuThrAlaIleLeuIleIle	205
QY	844	ATAGTCCCTGGAGTTATGAGCTAATTAAGGTCAAACGCAACTTTTAAAGACGCTTT	903
DB	206	IleValProGlyValMetGlnLeuIleLysGlyGlnThrGlnAsnPheLysAlaPhe	225
QY	904	TCAGAAAGAGANTCAAGTATACCGGTTGCGCTTTTATATGGAATGATGCA	963
DB	226	SerGlyArgSerSerIleThrArgLeuProLeuAlaPheTyrTyrGlyMetTyrAla	245
QY	964	TATGCTGCTGCTTTTACTCACTTGTACTGAGAGAGTGAACCCCTGAAAAACC	1023
DB	246	TyrAlaGlyTrpPheTyrLeuAsnPheValThrGluGluValGluAsnProGluLysThr	265
QY	1024	ATTCCTCTGCAATATGATATCCATGCGCATTTGTCACCATTTGCTGTGCAAAAT	1083
DB	266	IleProLeuAlaIleCysIleSerMetAlaIleValThrIleGlyTyrValLeuThrAsn	285
QY	1084	GTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTCAATGCAATGCGAGTG	1143
DB	286	ValAlaTyrPheThrThrIleAsnAlaGluGluLeuLeuLeuSerAsnAlaValAlaVal	305

QY	1144	ACCTTTTCTGAGCGGCTACTGGGAATTTCTCATTACAGTTCGATCTTTGTTGCCCTC	1203
DB	306	ThrPheSerGluArgLeuLeuGlyAsnPheSerLeuAlaValProIlePheValAlaLeu	325
QY	1204	TCCTGTCTTGGCTCCCATGAACGGTGTGTGTTGCTGTCTCCAGGTTATCTATGTTGCG	1263
DB	326	SerCysPheGlySerMetAsnGlyGlyValPheAlaValSerArgLeuPheTyrValAla	345
QY	1264	TCCTGAGAGGTCACCTTCAGAAATCCTCTCCATGATTCATGTCGCGAAGCACTCCT	1323
DB	346	SerArgGluGlyHisLeuProGluIleLeuSerMetIleHisValArgLysHisThrPro	365
QY	1324	CTACCAAGCTGTATTTGTTTGCACCTTTCACATGATGATGATGATGATGATGATGATG	1383
DB	366	LeuProAlaValIleValLeuHisProLeuThrMetIleMetLeuPheSerGlyAspLeu	385
QY	1384	GACAGCTCTTTGAATTTCTCAGTTTTCCTGAGTGGCTTTTATTTGGGCTGGCAGTTGCT	1443
DB	386	AspSerLeuLeuAsnPheLeuSerPheAlaArgTyrLeuPheIleGlyLeuAlaValAla	405
QY	1444	GGCTGATTTATCTTGATACAAATGCCAGATATGCATGCTCTTTCAGGTCGCACTG	1503
DB	406	GlyLeuIleTyrLeuArgTyrLysCysProAspMetHisArgProPheLysValProLeu	425
QY	1504	TTCATCCAGCTTTGTTTCTTTCACATGCTCTTCAATGTTTGCCTTCCCTCTATTGCG	1563
DB	426	PheIleProAlaLeuPheSerPheThrCysLeuPheMetValAlaLeuSerLeuTyrSer	445
QY	1564	GACCCATTTAGTACAGGATTTGCTGCTCATCTGACTGAGTCCCTGCGGTATAT	1623
DB	446	AspProPheSerThrGlyIleGlyPheValIleThrLeuThrGlyValProAlaTyrTyr	465
QY	1624	CTCTTTATATATGGAACCAACCCAGTGTGTGATGATGATGATGATGATGATGATGATG	1683
DB	466	LeuPheIleIleTrpAspLysLysProArgTrpPheArgIleMetSerGluLysIleThr	485
QY	1684	AGACATTTACAAATAATCTGGAAGTTGTACCAAGAGAGATAAGTTA	1731
DB	486	ArgThrLeuGlnIleIleLeuGluValValProGluLysPheLeu 501	

## RESULT 3

US-10-214-867A-13  
; Sequence 13, Application US/10214867A  
; Publication No. US2003014844A1  
; GENERAL INFORMATION:  
; APPLICANT: ENDOU, HITOSHI  
; TITLE OF INVENTION: SODIUM-INDEPENDENT SMALL NEUTRAL AMINO ACID  
; TITLE OF INVENTION: TRANSPORTERS TRANSPORTING L- AND D-AMINO ACIDS AND  
; FILE REFERENCES: 57783 (71526)  
; CURRENT APPLICATION NUMBER: US/10/214,867A  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: PCT/JP01/00031  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: JP 2000-28822  
; PRIOR FILING DATE: 2000-02-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Murine sp.  
US-10-214-867A-13

Alignment Scores:  
Pred. No.: 1,64e-207 Length: 502  
Score: 2298.00 Matches: 443  
Percent Similarity: 92.82% Conservative: 35  
Best Local Similarity: 86.02% Mismatches: 19  
Query Match: 55.78% Indels: 18  
DB: 12 Gaps: 1

US-09-667-170A-440 (1-2239) x US-10-214-867A-13 (1-502)

184	QY	AAGCTGTGTCACCATCTCCAAAGGAGGTACCTCGAGGAAATGTTAACGGAGG	243
		:::     :::     :::     :::     :::     :::	
4	Db	LysProValValAlaThrIleSerLysGlyGlyTyrLeuGlnGlyAsnMetSerGlyArg	23
		:::     :::     :::     :::     :::     :::	
244	QY	CTGCCTTCCCTGGGCAACAAGAGGCCACTCGGGCAGGACGCCCTTTTCAGGAAGAGCGCC	303
		:::     :::     :::     :::     :::     :::	
24	Db	LeuProSerMetGlyAspGlnGluProProGlyGln-----	35
		:::     :::     :::     :::     :::     :::	
304	QY	TTTTTCAGGAGAGACGCCCTTTTCAGGAAGAGAGAAGTGCGAGCTGAAGAGGAAGTCACCT	363
		:::     :::     :::     :::     :::     :::	
36	Db	-----GlnLysValValLeuLysLysLysIleThr	45
		:::     :::     :::     :::     :::     :::	
364	QY	TTACTGAGGGAGTCTCTATTATCATTGGCACCATCATTTGAGCAGAAATCTTCATCTCT	423
		:::     :::     :::     :::     :::     :::	
46	Db	LeuLeuArgGlyValSerIleIleGlyThrValIleGlySerGlyIlePheIleSer	65
		:::     :::     :::     :::     :::     :::	
424	QY	CCTTAAGGGCTGCTCCAGAACACGGGCGAGCGTGGGCATGTCTCTGACCATCTCGACGGTG	483
		:::     :::     :::     :::     :::     :::	
66	Db	ProLysGlyIleLeuGlnAsnThrGlySerValGlyMetSerLeuValPheTrpSerAla	85
		:::     :::     :::     :::     :::     :::	
484	QY	TGTGGGCTCTGTCACATATTTGGAGCTTTGTCTTATCTCAATTGGGAAACAATAAAG	543
		:::     :::     :::     :::     :::     :::	
86	Db	CysGlyValLeuSerLeuPheGlyAlaLeuSerTyrAlaGluLeuGlyThrSerIleLys	105
		:::     :::     :::     :::     :::     :::	
544	QY	AAATCTGGAGGTCAATACATATATTTTGGAGTCTTTGGTCATACACAGCTTTTGTA	603
		:::     :::     :::     :::     :::     :::	
106	Db	LysSerGlyHisTyrThrTyrIleLeuGluValPheGlyProLeuLeuAlaPheVal	125
		:::     :::     :::     :::     :::     :::	
604	QY	CGAGTCTGGGTGAACTCCATCAATAAGCCCTCGACGTACTGCTGTGATATCCCTGGCA	663
		:::     :::     :::     :::     :::     :::	
126	Db	ArgValTrpValGluLeuLeuValIleArgProGlyAlaThrAlaValIleSerLeuAla	145
		:::     :::     :::     :::     :::     :::	
664	QY	TTTGGACGTACATTCGTGGAACCATTTTTTATCAATGTCAAATCCCTGAACTTGCATC	723
		:::     :::     :::     :::     :::     :::	
146	Db	PheGlyArgTyrIleLeuGluProPhePheIleGlnCysGluIleProGluLeuAlaIle	165
		:::     :::     :::     :::     :::     :::	
724	QY	AGCTCATACAGTGTGGGCATTAACATGTAGTAGTGCTCTTAATACATGAGTGTGACG	783
		:::     :::     :::     :::     :::     :::	
166	Db	LysLeuValThrAlaValGlyIleThrValValMetValLeuAsnSerThrSerValSer	185
		:::     :::     :::     :::     :::     :::	
784	QY	TGAGAGCCCGGATCCAGATTTTCTTAACCTTTTTCAGAGTCCACAGCAATCTCATTAAT	843
		:::     :::     :::     :::     :::     :::	
186	Db	TrpSerAlaArgIleGlnIlePheLeuThrPheCysIleuThrAlaIleLeuIleIle	205
		:::     :::     :::     :::     :::     :::	
844	QY	ATAGTCCTCGAGTTATGCACTAATTAAGGTCAAAACGCGAGAACTTTAAAGACGCCCTTT	903
		:::     :::     :::     :::     :::     :::	
206	Db	IleValProGlyValIleGlnLeuIleLysGlyGlnThrHisPheLysAspAlaPhe	225
		:::     :::     :::     :::     :::     :::	
904	QY	TCAGGAGAGATCAAGTATTACGGGTTGCCATGCTTTTATTATGGAATGATGCA	963
		:::     :::     :::     :::     :::     :::	
226	Db	SerGlyArgAspThrSerLeuMetGlyLeuProLeuAlaPheTyrTyrGlyMetTyrAla	245
		:::     :::     :::     :::     :::     :::	
964	QY	TATGCTGCTGGTTTATCCCTCAACTTTGTACTGAAGAAGTAGAAAAACCTGAAAAAAC	1023
		:::     :::     :::     :::     :::     :::	
246	Db	TyrAlaGlyTrpPheTyrLeuAsnPheIleThrGluValAspAsnProGluLysThr	265
		:::     :::     :::     :::     :::     :::	
1024	QY	ATTCCCCTTCGATATGTTATTCATCGGCATTTGTCACCATTTGGCTATGCTGACAAAT	1083
		:::     :::     :::     :::     :::     :::	
266	Db	IleProLeuAlaIleCysIleSerMetAlaIleIleThrValGlyTyrValLeuThrAsn	285
		:::     :::     :::     :::     :::     :::	
1084	QY	GTCGCCCTACTTTACGACCATTAAGTCGTGAGAGCTGCTGCTTCCAATCGAGTGGCAGTG	1143
		:::     :::     :::     :::     :::     :::	
286	Db	ValAlaTyrPheThrThrIleSerAlaGluLeuLeuGlnSerSerAlaValAlaVal	305
		:::     :::     :::     :::     :::     :::	
1144	QY	ACCTTTTCTCAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTCGCCCTC	1203
		:::     :::     :::     :::     :::     :::	
306	Db	ThrPheSerGluArgLeuLeuGlyLysPheSerLeuAlaValProIlePheValAlaLeu	325
		:::     :::     :::     :::     :::     :::	
1204	QY	TCTTGCTTTGGCTCCATGAACGGTGGTGTGTTCCTGCTCCAGGTTATCTATGTTGCG	1263
		:::     :::     :::     :::     :::     :::	



Db 70 LeuAsnGlyValAlaIleValGlyThrIleGlySerGlyIlePheValThrPro 89  
QY 427 AAGGCGTGTCCAGAACACGCGGAGCGTGGCATGCTCTGACCATCTGACCGGTGTGT 486  
Db 90 ThrGlyValLeuLeuGlySerProGlyLeuAlaLeuValValThrAlaAlaCys 109  
QY 487 GGGTCTGTCTACTATTGGAGCTTTGCTTATGCTGAATTGGGAACAACTATAAGAAA 546  
Db 110 GlyValPheSerIleValGlyAlaLeuCysTyrAlaGluLeuGlyThrThrIleSerLys 129  
QY 547 TCTGAGCTCATTACACATATATTGGAGCTTTGGTGGTTCATTACAGCTTTGTACGA 606  
Db 130 SerGlyGlyAspTyrAlaTyrMetLeuGluValTyrGlySerLeuProAlaPheLeuLys 149  
QY 607 GTCTGGTGGAACTCCTCATATACGCTCGAGCTACTGTGTGATATCCTCGCATTT 666  
Db 150 LeuTrpIleGluLeuLeuIleIleArgProSerSerGlnTyrIleValAlaLeuValPhe 169  
QY 667 GGAGCTCATCTTGGAAACCAATTTTATTCAATGTGAATCCCTGAACTTGGCATCAAG 726  
Db 170 AlaThrTyrLeuLeuLysProLeuPheProThrCysProValProGluGluAlaLys 189  
QY 727 CTCATTACAGCTGTGGGCACTACTGTAGTGTCTTAATAGCATGAGTGTGAGCTGG 786  
Db 190 LeuValAlaCysLeuCysValLeuLeuLeuThrAlaValAsnCysTyrSerValLysAla 209  
QY 787 AGGCGCCGATCCAGATTTCTTAACCTTTTGGCAAGCTCACAGCAATTTCTGATATATA 846  
Db 210 AlaThrArgValGlnAspAlaPheAlaAlaLysLeuLeuAlaLeuAlaLeuIle 229  
QY 847 GTCCCTGAGTTATGACACTAATTAAGTCAACGCGAGACTTTAAAGACGCTTTTCA 906  
Db 230 LeuLeuGlyPheValGlnIleGlyLysGlyAspValSerAsnLeuAspProAsnPheSer 249  
QY 907 -----GGAAGAGATTCAAGTATACGGGTGCTTATGGAATGTAT 960  
Db 250 PheGluGlyThrLysLeuAspValGlyAsnIleValLeuAlaLeuTyrSerGlyLeuPhe 269  
QY 961 GCATATGCTGGTGTGTTTACTCAACTTTGTTACTGAAGAGTAGAAGAACCTTCAAAA 1020  
Db 270 AlaTyrGlyGlyTyrAsnTyrLeuAsnPheValThrGluGluMetIleAsnProTyrArg 289  
QY 1021 ACCATTCCCTTGCATATGATATCCATGCTGCTTGTACCATGCTGCTATGCTGTACA 1080  
Db 290 AsnLeuProLeuAlaIleIleSerLeuProIleValThrLeuValTyrValLeuThr 309  
QY 1081 AATGTGGCTACTTTACACCAATTAATCTGAGAGCTGCTGCTTCAAAAGCAGTGCA 1140  
Db 310 AsnLeuAlaTyrPheThrThrLeuSerThrGluGlnMetLeuSerSerGluAlaValAla 329  
QY 1141 GTGACCTTTCTGAGCGGCTACTGGAAATTTCTCATTAGCAGTTCGATCTTTGTGCC 1200  
Db 330 ValAspPheGlyAsnTyrHisLeuGlyValMetSerTrpIleIleProValPheValGly 349  
QY 1201 CTCTCTGCTTGTGCTCCTCAAGCTGTGCTGTGCTGCTCAGGTTATCTATGTT 1260  
Db 350 LeuSerCysPheGlySerValAsnGlySerLeuPheThrSerSerArgLeuPhePheVal 369  
QY 1261 CGGTCTCGAGAGGTTCACCTTCCGAAATCTCTCCATGATTCATGTCCGCAACCACT 1320  
Db 370 GlySerArgGluGlyHisLeuProSerIleLeuSerMetIleHisProGlnLeuLeuThr 389  
QY 1321 CCTCTACAGCTGTATTGTTTGGACCCCTTGCATGATGATAATGCTCTTCTCGGAGAC 1380  
Db 390 ProValProSerLeuValPheThrCysValMetThrLeuLeuTyrAlaPheSerLysAsp 409  
QY 1381 CTCGACAGCTCTTTCAATTTCTCAGTTTCCAGGTGGCTTTTATGGCTGGCAGTT 1440  
Db 410 IlePheSerValIleAsnPhePheSerPhePheAsnTrpLeuCysValAlaLeuAlaIle 429  
QY 1441 GCTGGCTGTATTATCTTCGATACAAATGCCAGATGATGCTGCTCTTCAAGTGCCA 1500

Db 430 IleGlyMetIleTrpLeuArgHisArgLysProGluLeuGluArgProIleLysValAsn 449  
QY 1501 CTGTTCATCCAGCTTGTGTTTCTTTCACATGCTCTTCATGTTGCCCTTTCCTCTAT 1560  
Db 450 LeuAlaLeuProValPhePheIleLeuAlaCysLeuPheLeuAlaValSerPheTrp 469  
QY 1561 TCGACCCCACTTATAGTACAGGATTGGCTTCTCATCTCTGACTGGAGTCCCTGCGTAT 1620  
Db 470 LysThrProValGluCysGlyIleGlyPheThrIleLeuSerGlyLeuProValTyr 489  
QY 1621 TAICTCTTTATTATATCGGACAGAAACCCAGGTGGTTTGAATAATGTGAGAAATA 1680  
Db 490 PhePheGlyValTrpTrpLysAsnLysProLysTrpLeuLeuGlnGlyIlePheSerThr 509  
QY 1681 ACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAAGAA 1722  
Db 510 ThrValLeuCysGlnLysLeuMetGlnValValProGlnGlu 523

## RESULT 6

US-10-163-866-38  
; Sequence 38, Application US/10163866  
; Publication No. US20030027188A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: SLICs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-080C  
; CURRENT APPLICATION NUMBER: US/10/163,866  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/338,733  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/357,600  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 507  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-163-866-38

Alignment Scores:  
Pred. No.: 7,25e-104 Length: 507  
Score: 1198.50 Matches: 231  
Percent Similarity: 65.79% Conservative: 94  
Best Local Similarity: 46.76% Mismatches: 166  
Query Match: 29.09% Indels: 3  
DB: 15 Gaps: 2

US-09-667-170A-440 (1-2239) x US-10-163-866-38 (1-507)

QY 247 CTTTCCCTGGCAACAGAGAGCCACCTGGCAGAGCCCTTTTCAGGAAGAGAGCGCTTT 306  
Db 14 ProValAlaGluGluLysGluAlaArgLysMetLeuAlaSerLysArgAlaAsp 33  
QY 307 TCAGGAAGAGAGCCCTTTTCAGGAAGAGAGAAAGTGCAGTGCAGAGAGAAAGTCACTTTA 366  
Db 34 GlyAlaAlaProAlaGlyGluGly---GluGlyValThrLeuGlnArgAsnIleThrLeu 52  
QY 367 CTGAGGGAGTCTCCATTATTCATTGGCACCATTATTGGAGCAGGAATCTTCATCTCTCCT 426  
Db 53 LeuAsnGlyValAlaIleIleValGlyAlaIleIleGlySerGlyIlePheValThrPro 72  
QY 427 AAGGGCGTGTCCAGAACACGGSCAGCGTGGGCGATCTCTGACCATCTGGACGGTGTGT 486  
Db 73 ThrGlyValLeuLysGluAlaGlySerProGlyLeuAlaLeuValMetTrpAlaAlaCys 92  
QY 487 GGGGTCTGTCTACTATTGGAGCTTGTCTTATGCTGAATTGGGAACAACATATAAGAAA 546

Db 93 GlyValPheSerIleValGlyAlaLeuCysTyrAlaGluLeuGlyThrThrIleSerLys 112  
QY 547 TCTGGAGTCAATACACATATATTTTGAAGTCTTTGGTCCATTACAGCTTTTGTACGA 606  
Db 113 SerGlyGlyAspTyrAlaTyrMetLeuGluValTyrGlySerLeuProAlaPheLeuLys 132  
QY 607 GTCTGGTGGAACTCCATATAAGCCCTGCAGCTACTGCTGTGATATCCCTGGCATTT 666  
Db 133 LeuTrpIleGluLeuLeuIleIleArgProSerGlnTyrIleValAlaLeuValPhe 152  
QY 667 GGACCTACATCTCGAACCACTTTTATTCAATGTGAAATCCCTGAACTTGGCATCAAG 726  
Db 153 AlaAlaTyrLeuLeuLysProLeuPheProThrCysProValProGluGluAlaLys 172  
QY 727 CTCATTACAGCTGGGCATACACTGTAGTGTCTTAATAGCATGAGTGTGAGTGG 786  
Db 173 LeuValAlaCysLeuCysValLeuLeuThrAlaValAsnCysTyrSerValLysAla 192  
QY 787 AGCCGCGGATCCAGATTTCTTAACCTTTTGCAGCTCACAGCAATTTCTGATAATATA 846  
Db 193 AlaThrArgValGlnAspAlaPheAlaAlaLysLeuLeuAlaLeuIleIle 212  
QY 847 GTCCCTGGAGTATGACAGCTAATTAAGGTCAACAGCGACACTTTAAAGACGCTTTCA 906  
Db 213 LeuLeuGlyPheValGlnIleGlyLysGlyAspValSerAsnLeuAspProAsnPheSer 232  
QY 907 -----GGAAGATTCAGATTTACGGGTGGCTGCCTGTTTATTATGGAATGAT 960  
Db 233 PheGluGlyThrLysLeuAspValGlyAsnIleValLeuAlaLeuTyrSerGlyLeuPhe 252  
QY 961 GCATATGCTGCTGCTTTTACTCACTCACTTGTACTGAAGAGTAGAAGAACCCCTGAAAA 1020  
Db 253 AlaTyrGlyTyrAsnTyrLeuAsnPheValThrGluMetIleAsnProTyrArg 272  
QY 1021 ACCATTCCCTTGAATGATATATCATGAGCTGCTGCTTCAATGAGTGGCA 1140  
Db 293 AsnLeuProLeuAlaIleIleSerLeuProIleValThrLeuValTyrValLeuThr 292  
QY 1141 GTGACCTTTCTGAGCGCTACTCGGAAATTTCTCATTAGCAGTCCGATCTTTGTTGCC 1200  
Db 313 ValAspPheGlyAsnTyrHisLeuGlyValMetSerTrpIleIleProValPheValGly 332  
QY 1201 CTCTCTGCTTTGCTCCATGAAGCGTGGTGTGTTGCTGTCTCCAGTTATTTATGTT 1260  
Db 333 LeuSerCysPheGlySerValAsnGlySerLeuPheThrSerSerArgLeuPhePheVal 352  
QY 1261 GCGTCTGAGAGGTCACTTCCAGAAATCCTCTCCATGATTATGTCGCGCAACACACT 1320  
Db 353 GlySerArgGluGlyHisLeuProSerIleLeuSerMetIleHisProGlnLeuLeuThr 372  
QY 1321 CCTACACAGCTGTTATGTTTTCACCCCTTTGACCAATGATAATGCTCTCTCTGGAGAC 1380  
Db 373 ProValProSerLeuValPheThrCysValMetThrLeuLeuTyrAlaPheSerLysAsp 392  
QY 1381 CTCGACAGCTTTTGAATTTCTCAGTTTTCGAGGTGGCTTTTATTTGGCTCGCAGTT 1440  
Db 393 IlePheSerValIleAsnPhePheSerPhePheAsnTrpLeuCysValAlaLeuAlaIle 412  
QY 1441 GCTGGCTGATTTATCTCGATACAAATGCCAGATATGATCGTCTCTTCAAGTGCCA 1500  
Db 413 IleGlyMetIleTrpLeuArgHisArgLysProGluLeuGluArgProIleLysValAsn 432  
QY 1501 CTGTTATCCAGCTTTGTTTCTTCATGCTCTTTCATGTTGTCCTTTCCTCTAT 1560  
Db 433 LeuAlaLeuProValPhePheIleLeuAlaCysLeuPheLeuIleAlaValSerPheTrp 452  
QY 1561 TCGGACCACTTTAGTACAGGATTTGGCTTCTCATCACTCTGACTGGAGTCCCTGGCTAT 1620

Db 453 LysThrProValGluCysGlyIleGlyPheThrIleIleLeuSerGlyLeuProValTyr 472  
QY 1621 TATCTCTTAT 1680  
Db 473 PhePheGlyValTrpTrpLysAsnLysProLysTrpLeuLeuGlnGlyIlePheSerThr 492  
QY 1681 ACCAGAACATTACAAATAATATCTGGAAGTTGTACCAAGAGAA 1722  
Db 493 ThrValLeuCysGlnLysLeuMetGlnValValProGlnGlu 506  
RESULT 7  
US-10-163-866-39  
; Sequence 36, Application US/10163866  
; Publication No. US20030027188A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: SLCTs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-080C  
; CURRENT APPLICATION NUMBER: US/10/163,866  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/338,733  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/357,600  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 39  
; LENGTH: 507  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-163-866-39  
Alignment Scores:  
Pred. No.: 7,25e-104 Length: 507  
Score: 1198.50 Matches: 231  
Percent Similarity: 65.79% Conservative: 94  
Best Local Similarity: 46.76% Mismatches: 166  
Query Match: 29.09% Indels: 3  
DB: 15 Gaps: 2  
US-09-667-170A-440 (1-2239) x US-10-163-866-39 (1-507)  
QY 247 CCTCTCCCTGGCAACAGGAGCCACCCTGGCAGAGCGCCTTTTCAGGAAGAGACGCCCTTT 306  
Db 14 ProValAlaGluGluLysGluGluAlaArgGluLysMetLeuAlaSerLysA-GalaAsp 33  
QY 307 TCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGAAAGTCACTTTA 366  
Db 34 GlyAlaAlaProAlaGlyGluGly---GluGlyValThrLeuGlnArgAsnIleThrLeu 52  
QY 367 CTGAGGGAGTCTCCATTATTCATTGCGCACCATTGAGCAGCAATCTTCATCTCTCCT 426  
Db 53 LeuAsnGlyValAlaIleIleValGlyAlaIleIleGlySerGlyIlePheValThrPro 72  
QY 427 AAGGGGTGCTCCAGAACACGGGCGAGCTGGGCGATGCTCTGACCATCTGAGCGGTGTGT 486  
Db 73 ThrGlyValLeuLysGluAlaGlySerProGlyLeuAlaLeuValMetTrpAlaAlaCys 92  
QY 487 GGGTCTCTGCTACTATTGAGCTTTGTCTTATGCTGAATTTGGAAACAACATATAAGAAA 546  
Db 93 GlyValPheSerIleValGlyAlaLeuCysTyrAlaGluLeuGlyThrThrIleSerLys 112  
QY 547 TCTGGAGTCAATACACATATATTTTGAAGTCTTTGGTCCATTACAGCTTTTGTACGA 606  
Db 113 SerGlyGlyAspTyrAlaTyrMetLeuGluValTyrGlySerLeuProAlaPheLeuLys 132  
QY 607 GTCTGGTGGAACTCCATATAATACCCCTGCAGCTACTGCTGTGATATCCCTGGCATTT 666





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QY 838 ATAATTATAGTCCCTGGAGTTATGACGACTAATAA-----GGTCAACGCGAG 885
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
211 LeuIleLeuLeuGlyPheIleGlnMetGlyLysAspIleGlyGlnGlyAspAlaSer 230
QY 886 AACITTT-----AAGACGCCCTTTTCAGGAGAGAGATTCAGTATTACGGGTGCGCATG 939
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
231 AsnLeuHisGlnLysLeuSerPheGluGlyThrAsnLeuAspValGlyAsnIleValLeu 250
QY 940 GCTTTTATTATGGAATGATCATGCTGCTGTTTACCTCAACTTGTACTGAA 999
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
251 AlaLeuTyrSerGlyLeuPheAlaIleGlyTyrAsnTyrLeuAsnPheValThrGlu 270
QY 1000 GAAGTAGAAACCCCTGAAAAACCAATCCCTTGCATATGATATATCCATGCGCATGTC 1059
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
271 GluMetIleAsnProTyrArgAsnLeuProLeuAlaIleIleSerLeuProIleVal 290
QY 1060 ACCATTGGCTATGCTGCAAAATGCGCTACTTACGACCAATTAATGCGAGGAGTC 1119
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
291 ThrLeuValTyrValLeuThrAsnLeuAlaTyrPheThrThrLeuSerThrAsnGlnMet 310
QY 1120 CTGCTTTCAAAATGCGAGTGGCAGTACCTTTCTGAGCGGCTACTGGGAAATTTCTCATTA 1179
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
311 LeuThrSerGluAlaValAlaValAspPheGlyAsnTyrHisLeuGlyValMetSerTrp 330
QY 1180 GCAGTTCGAGTCTTTGTGCGCTCTCTGCTTGGCTCCATGAACGGGTGTGTGCT 1239
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
331 IleIleProValPheValGlyLeuSerCysPheGlySerValAsnGlySerLeuPheThr 350
QY 1240 GTCTCCAGGTATTATGTTGCGTCTCGAGAGGTCTACCTTCCAGAAATCTCTCCATG 1299
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
351 SerSerArgLeuPhePheValGlySerArgGluGlyHisLeuProSerIleLeuSerMet 370
QY 1300 ATTCTATGCCGACGACACTCTCTACGAGTGTATTGTTTTCACCCCTTTGCAATG 1359
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
371 IleHisProGlnLeuLeuThrProValProSerLeuValPheThrCysValMetThrLeu 390
QY 1360 ATAATGCTCTCTCTGGAGACTCGACAGTCTTTTGAATTCCTCAGTTTTCGCCAGGTG 1419
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
391 MetTyrAlaPheSerArgAspIlePheSerIleIleAsnPhePheSerPhePheAsnTrp 410
QY 1420 CTTTATTATGGCTGCGCTGCTGGCTGATTATCTTCGNATCAAAATGCCAGATATG 1479
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
411 LeuCysValAlaLeuAlaIleIleGlyMetTrpLeuArgPheLysLysProGlnLeu 430
QY 1480 CATGCTCTTTCAAGTGCACCTGTCATCCAGCTTTGTTTCTTCCATGCTCTCTC 1539
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
431 GluArgProIleLysValAsnLeuAlaLeuProValPhePheIleLeuAlaCysLeuPhe 450
QY 1540 ATGGTTGCGCTTTCCTCTATTTCGACCCATTTAGTACAGGATTGGCTTCGTATCACT 1599
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
451 LeuIleAlaValSerPheTrpIlyThrProLeuGluCysGlyIleGlyPheAlaIleIle 470
QY 1600 CTGACTGAGTCCCTCGCTATTATCTTTATATATGGACAAACCCAGGTGGTTT 1659
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
471 LeuSerGlyLeuProValTyrPheGlyValTrpTrpLysAsnLysProLysTrpIle 490
QY 1660 AGAATAATGTCAGAGAAATACCAAGAACATTAACAAATGGAAGTGTACAGAA 1719
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
491 LeuGlnValIlePheSerValThrValLeuCysGlnLysLeuMetCysValValProGln 510
QY 1720 GAA 1722
Db ::::
511 Glu 511
```

## RESULT 9

US-10-214-867A-12

; Sequence 12, Application US/10214867A

; Publication No. US2003014844A1

; GENERAL INFORMATION:

; APPLICANT: HITOSHI

; APPLICANT: KANAI, YOSHIKATSU

; TITLE OF INVENTION: SODIUM-INDEPENDENT SMALL NEUTRAL AMINO ACID

; ; TITLE OF INVENTION: TRANSPORTERS TRANSPORTING L- AND D-AMINO ACIDS AND

```
; TITLE OF INVENTION: GENES THEREOF
; FILE REFERENCE: 57783 (71526)
; CURRENT APPLICATION NUMBER: US/10/214,867A
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00031
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: JP 2000-28822
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 12
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-214-867A-12
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## Alignment Scores:

Pred. No.:	6.64e-100	Length:	515
Score:	1156.50	Matches:	218
Percent Similarity:	69.16%	Conservative:	105
Best Local Similarity:	46.68%	Mismatches:	141
Query Match:	28.07%	Indels:	3
DB:	12	Gaps:	2

US-09-667-170A-440 (1-2239) x US-10-214-867A-12 (1-515)

QY	334	GAGAAAGTCGACGTGAGAGAAAGTCACTTTACTGAGGGAGTCTCATATATCATTGGC	393
Db	37	GluThrMetGlnLeuLysLysGluIleSerLeuLeuAsnGlyValSerLeuValValGly	56
QY	394	ACCATCATTTGAGCAGGAAATCTTCATCTCTCTAAGGCGCTCCAGAACACGCGGACG	453
Db	57	AsnMetIleGlySerGlyIlePheValSerProLysGlyValLeuValHisThrAlaSer	76
QY	454	GTGGGCTGCTCTGACACATCTGACGCGTGTGGGTCTGTCTGCTCACTATTGGAGCTTG	513
Db	77	TyrglyMetSerLeuIleValTrpAlaIleGlyLeuPheSerValValGlyAlaLeu	96
QY	514	TCTTATCTGAATGGCAACAATTAAGAAATCTGAGGTCTGAGTCAATACACATATTTTG	573
Db	97	CysTyrAlaGluLeuGlyThrThrIleThrLysSerGlyAlaSerTyrAlaTyrIleLeu	116
QY	574	GAACTCTTTGTCCTTACCAGCTTTTGTACGAGTCTGGGTGGAACTCTCATATAATACG	633
Db	117	GluAlaPheGlyGlyPheIleAlaPheIleArgLeuTrpValSerLeuLeuValGlu	136
QY	634	CTCGACGCTACTGCTGTGATATCCCTGGCATTTGGACGTACATCTGGAACCAATTTT	693
Db	137	ProThrGlyGlnAlaIleAlaIleThrPheAlaAsnTyrIleIleGlnProSerPhe	156
QY	694	ATTCAATGTGAATCCCTGAACTTGGCATCAAGCTCAATACAGCTGTGGGCATTAAGTGA	753
Db	157	ProSerCysAspProTyrLeuAlaCysArgLeuLeuAlaAlaCysIleCysLeu	176
QY	754	GTGATGTCCTTAATAGCATGAGTGTGAGTGGAGCGCCCGGATCCAGATTTCTTAACC	813
Db	177	LeuThrPheValAsnCysAlaTyrValLysTrpGlyThrArgValGlnAspThrPheThr	196
QY	814	TTTTCGAGCTCAGCAATTCGATAATTATAGTCTCTCGAGGTATGCGACTAATTA	873
Db	197	TyrAlaLysValValAlaLeuIleAlaIleValMetGlyLeuValLysLeuCysGln	216
QY	874	GGTCAACGCGAGAACTTTAAAGACGCTTTTCAGGAAGAGATTCAAGTATTACCGGTTG	933
Db	217	GlyHisSerGluHisPheGlnAspAlaPheGluGlySerSerTrpAspMetGlyAsnLeu	236
QY	934	CCACTGGCTTTTATTATGAATGTATGCATATGCTGCTGGTGGTTTACCTCAACTTGT	993
Db	237	SerLeuAlaLeuTyrSerAlaLeuPheSerTyrSerGlyTrpAspThrLeuAsnPheVal	256
QY	994	ACTGAGAGTAGAAACCTTGAAAAACCATTCCTCCCTTCGAATATATATCATCATGCC	1053
Db	257	ThrGluGluIleLysAsnProGluArgAsnLeuProLeuAlaIleGlyIleSerMetPro	276





QY 1234 TTTGCTGCTCCAGGTTATTCTATGTTGGCTCTCGAGAGGTCACCTTCAGAAATCCTC 1293  
DB 337 PheAlaSerArgLeuPheValGlySerArgGluGlyHisLeuProAspLeuLeu 356  
QY 1294 TCCATGATTTCATGCCCAAGCACACTCCTCTACAGCTGTATTGTTTGCACCCCTTG 1353  
DB 357 SerMetIleHisIleGluArgPheThrProIleProAlaLeuLeuPheAsnCysThrMet 376  
QY 1354 ACAATGATAATGCTCTCTCTGGAGACTCGACAGTCTTTTGAAATTCCTCAGTTTGGC 1413  
DB 377 AlaLeuIleTyrLeuIleValGluAspValPheGlnLeuIleAsnTyrPheSerPheSer 396  
QY 1414 AGGTGGCTTTTATTGGCTGGCAGTTGCTGGCTGATTATCTTCGATACAAATGCCA 1473  
DB 397 TyrTrpPheIleValGlyLeuSerValGlyGlnLeuTyrLeuArgTrpLysGluPro 416  
QY 1474 GATATGATCGCTCTCAAGTGCCACTGTCTATCCAGCTTTGTTTCTCCATGC 1533  
DB 417 LysArgProArgProLeuLysLeuSerValPhePheProIleValPheCysSer 436  
QY 1534 CTCTTCAGTTGGCTTCTCCTCTATTCGACCCATTTAGTACAGGATTTGGCTTGGTC 1593  
DB 437 ValPheLeuValIleValProLeuPheThrAspThrIleAsnSerLeuIleGlyIleGly 456  
QY 1594 ATCACTCTGACTGGAGTCCCTGGCTGATTATCTC-----TTTATTATGGGCAAGAAA 1647  
DB 457 IleAlaLeuSerGlyValProPheTyrPheMetGlyValTyrLeuProGluSerArgArg 476  
QY 1648 CCCAGTGGTTTAGAATAATCTCAGAGAAAATAACCAGA---ACATTACAATAATACTG 1704  
DB 477 ProLeuPheIleArgAsnValLeuAlaAlaIleThrArgGlyThrGlnGlnLeuCysPhe 496  
QY 1705 GAAGTTGTACAGAGAGAT 1725  
DB 497 CysValLeuThrGluLeuAsp 503

## RESULT 11

US-10-163-866-41  
; Sequence 41, Application US/10163866  
; Publication No. US20030027188A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-080C  
; CURRENT APPLICATION NUMBER: US/10/163,866  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/338,733  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/357,600  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 41  
; LENGTH: 511  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-163-866-41

Alignment Scores:  
Pred. No.: 1,51e-97 Length: 511  
Score: 1131.50 Matches: 214  
Percent Similarity: 68.00% Conservative: 109  
Best Local Similarity: 45.05% Mismatches: 149  
Query Match: 27.46% Indels: 3  
DB: 15 Gaps: 2

US-09-667-170A-440 (1-2239) x US-10-163-866-41 (1-511)

QY 310 GGAAGAGAGCGCTTTTCAGAGAGAGAAAGTCACTGAGAGAGAAAGTCACTTTACTG 369  
DB 21 GlyAspGlyAlaSerProGlyProGluGlnValLysLeuLysGluIleSerLeuLeu 40  
QY 370 AGGGAGTCTCCATTCATTTGGCACCATCATTGGAGCAGGAATCTTCATCTCTCCCTAAG 429  
DB 41 AsnGlyValCysLeuIleValGlyAsnMetIleGlySerGlyIlePheValSerProLys 60  
QY 430 GGGTGTCTCCAGAACACGGGCGACGCTGGCGCATCTCTGACCATCTGGACGGTGTGGGG 489  
DB 61 GlyValLeuIleTyrSerAlaSerPheGlyLeuSerLeuValIleTrpAlaValGlyGly 80  
QY 490 GTCCTGTCACTATTTCGAGCTTTGTCTTATCGGAATTGGGAACAACATAAAGAAATCT 549  
DB 81 LeuPheSerValPheGlyAlaLeuCysTyrAlaGluLeuGlyThrThrIleLysLysSer 100  
QY 550 GGAGGTCAATTACACATATATTTTGGGAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTC 609  
DB 101 GlyAlaSerTyrAlaTyrIleLeuGluAlaPheGlyGlyPheLeuAlaPheIleArgLeu 120  
QY 610 TGGGTGGAATCTCTCATATATACCCCTGAGCTACTGCTGATATCCCTGGCATTTTGA 669  
DB 121 TrpThrSerLeuLeuIleIleGluProThrSerGlnAlaIleIleAlaIleThrPheAla 140  
QY 670 CGCTACATCTCGAACCATTTTATTCAATGTGAAATCCCTGAACTTGGCATCAAGCTC 729  
DB 141 AsnTyrMetValGlnProLeuPheProSerCysPheAlaProTyrAlaAlaSerArgLeu 160  
QY 730 ATTACAGCTGTGGGCATTAACCTAGTAGTGTCTTAATAGCATGTGTGTCAGCTGGAGC 789  
DB 161 LeuAlaAlaAlaCysIleCysLeuLeuThrPheIleAsnCysAlaTyrValLysTyrGly 180  
QY 790 GCCGGATCCAGATTTTCTTAACCTTTTGAAGCTCACACAATCTGATATATATATGTC 849  
DB 181 ThrLeuValGlnAspIlePheThrTyrAlaLysValLeuAlaLeuIleAlaValIleVal 200  
QY 850 CTTGGAGTTATGACAGCTAAATTAAGGTCAACAGCAGAACTTTAAAGACGCTTTTCAGGA 909  
DB 201 AlaGlyIleValargLeuGlyGlnGlyAlaSerThrHisPheGluAsnSerPheGluGly 220  
QY 910 AGAGATTCAAGTATTACCGGGTCCCATCGCTGCTTTTATTATGAATGTATGATATGCT 969  
DB 221 SerSerPheAlaValAlaGlyAspIleAlaLeuAlaLeuTyrSerAlaLeuPheSerTyrSer 240  
QY 970 GGCTGGTTTACCTCAACTTGTGTACTGAAGAGTAGAAGAACCTGAAAAACCATTTCCC 1029  
DB 241 GlyTrpAspThrLeuAsnTyrValThrGluIleLysAsnProGluLysArgLeuPro 260  
QY 1030 CTTGCAATATGTATATCCATGGCCATTGTCAACCATTTGGCTATGTCTGACAAAATGTGGCC 1089  
DB 261 LeuSerIleGlyIleSerMetProIleValThrIleIleTyrIleLeuThrAsnValAla 280  
QY 1090 TACTTTAGACCAATTAAGTGTAGGAGCTGCTGCTTTCAATATGAGTGGAGTACCTTTT 1149  
DB 281 TyrTyrThrValLeuAspMetArgAspIleLeuAlaSerAspAlaValAlaValThrPhe 300  
QY 1150 TCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCGGATCTTTGTTGGCTCTCTGTC 1209  
DB 301 AlaAspGlnIlePheGlyIlePheAsnTrpIleIleProLeuSerValAlaLeuSerCys 320  
QY 1210 TTTGGCTCCATGAACGGTGGTGTGTTTGTCTGTCTCCAGGTTATTCTATGTTGCTCTCGA 1269  
DB 321 PheGlyLeuAsnAlaSerIleValAlaAlaSerArgLeuPheValGlySerArg 340  
QY 1270 GAGGTCACTTCCAGAAATCTCTTCCATGATTTCATCTCCGACAGACACTCTCTACCA 1329  
DB 341 GluGlyHisLeuProAspAlaIleCysMetIleHisValGluArgPheThrProValPro 360  
QY 1330 GCTGTTATTGTTTGGACCCCTTTGACAAATGATATGCTCTTCTCTGGAGACCTCGACAGT 1389  
DB 361 SerLeuLeuPheAsnGlyIleMetAlaLeuIleTyrLeuCysValGluAspIlePheGln 380



US-10-163-866-43

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; Sequence 43, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLCT's AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-163-866-43

Alignment Scores:
Pred. No.: 1,03e-94 Length: 535
Score: 1101.50 Matches: 220
Percent Similarity: 65.52% Conservative: 103
Best Local Similarity: 44.62% Mismatches: 161
Query Match: 26.74% Indels: 9
Dbs: 15 Gaps: 4

US-09-667-170A-440 (1-2239) x US-10-163-866-43 (1-535)

QY 262 AAGGAGCCACCTGGGAGGAGCGCTTTTCAGGAGAGAGCGCTTTTCAGGAGAGAGCGCC 321
DB 13 LysLysHisProGly-----GlyGlyGlySerAspAlaSerProGluAla 27
QY 322 TTTTCAGGAGAGAGAAAGTGCAGTGAAGAGAAAGTCACTTTACTAGAGGGAGTCTCC 381
DB 28 GlySerGlyGlyGlyValAlaLeuLysGlyLeuValSerAlaCysGly 47
QY 382 ATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCACTCTCCTAAGGCGTGTCCAG 441
DB 48 IleIleValGlyAsnIleIleGlySerGlyIlePheValSerProLysGlyValLeuGlu 67
QY 442 AACACGGGAGCGTGGGAGTGTCTGTGACCATCTGGACGGTGTGTGGGTCTGTGCTACTA 501
DB 68 AsnAlaGlySerValGlyLeuAlaLeuIleValTrpIleValThrGlyPheIleThrVal 87
QY 502 TTTGAGCTTTGCTTATGCTGAATGGGAACAATATAAGAAATCTGGAGGTCAATTAC 561
DB 88 ValGlyAlaLeuCysTyrAlaGluLeuGlyValThrIleProLysSerGlyGlyAspTyr 107
QY 562 ACATATATTTTGGAGTCTTGTGCTCCATACAGCTTTGTACGAGTCTGGTGGAACTC 621
DB 108 SerTyrValLysAspIlePheGlyLeuAlaGlyPheLeuArgLeuTrpIleAlaVal 127
QY 622 CTCAATACGCGCTGAGTACTGCTGTGATATCCCTGGCATTTGGAGCGGTACATTCTG 681
DB 128 LeuValIleTyrProThrAsnGlnAlaValIleAlaLeuThrPheSerAsnTyrValLeu 147
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## RESULT 15

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US-10-163-866-44
; Sequence 44, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLCT's AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05

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GenCore version 5.1.6  
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# SUMMARIES

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158	19	0.8	936	2	US-08-557-309B-21	Sequence 21, Appl	c 231	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
159	19	0.8	936	3	US-08-824-306-21	Sequence 21, Appl	c 232	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
160	19	0.8	936	3	US-08-993-674A-21	Sequence 21, Appl	c 233	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
161	19	0.8	936	4	US-09-256-976-21	Sequence 21, Appl	c 234	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
162	19	0.8	959	4	US-09-205-258-19	Sequence 19, Appl	c 235	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
163	19	0.8	1001	4	US-09-641-638-208	Sequence 208, App	c 236	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
164	19	0.8	1001	4	US-03-641-638-292	Sequence 292, App	c 237	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
165	19	0.8	1100	3	US-08-248-335-53	Sequence 53, App	c 238	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
166	19	0.8	1120	1	US-08-188-582-8	Sequence 8, Appl	c 239	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
167	19	0.8	1120	1	US-08-646-715-8	Sequence 8, Appl	c 240	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
168	19	0.8	1189	4	US-09-369-347-22	Sequence 22, Appl	c 241	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
169	19	0.8	1268	4	US-09-369-247-42	Sequence 42, Appl	c 242	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
170	19	0.8	1290	3	US-09-289-349-9	Sequence 9, Appl	c 243	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
171	19	0.8	1312	2	US-08-580-545B-9	Sequence 9, Appl	c 244	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
172	19	0.8	1312	3	US-09-262-653A-9	Sequence 9, Appl	c 245	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl
173	19	0.8	1347	3	US/08/622	INFORMATION FOR	c 246	19	0.8	1837	3	US-09-352-302-3	Sequence 3, Appl



247	19	0.8	3883	1	US-08-468-036-33	Sequence 33, Appl	320	19	0.8	10881	4	US-09-357-206A-9	Sequence 9, Appl
248	19	0.8	3883	2	US-08-376-843-33	Sequence 33, Appl	C 321	19	0.8	12143	4	US-09-423-744A-1	Sequence 1, Appl
249	19	0.8	3884	3	US-09-541-782-3	Sequence 3, Appl	322	19	0.8	12146	4	US-09-277-457-27	Sequence 27, Appl
250	19	0.8	3884	4	US-09-723-820-3	Sequence 3, Appl	323	19	0.8	12146	4	US-09-679-729-27	Sequence 27, Appl
251	19	0.8	4084	3	US-08-866-340-1	Sequence 8, Appl	324	19	0.8	12386	4	US-09-357-206A-1	Sequence 1, Appl
252	19	0.8	4281	4	US-09-357-206A-8	Sequence 8, Appl	C 325	19	0.8	12597	4	US-09-705-299-12	Sequence 12, Appl
253	19	0.8	4352	4	US-09-620-312D-555	Sequence 555, App	C 326	19	0.8	13011	2	US-08-791-849A-14	Sequence 14, Appl
254	19	0.8	4460	4	US-09-103-875-4	Sequence 4, Appl	C 327	19	0.8	14747	4	US-09-608-285A-42	Sequence 42, Appl
255	19	0.8	4519	3	US-08-456-200B-2	Sequence 2, Appl	C 328	19	0.8	14747	4	US-09-557-800C-42	Sequence 42, Appl
256	19	0.8	5109	4	US-08-930-055A-2	Sequence 2, Appl	C 329	19	0.8	15977	4	US-09-608-285A-59	Sequence 59, Appl
257	19	0.8	5208	3	US-08-781-891-70	Sequence 70, Appl	C 330	19	0.8	17000	4	US-09-679-299A-18	Sequence 18, Appl
258	19	0.8	5208	4	US-09-791-211-11	Sequence 11, Appl	C 331	19	0.8	18073	3	US-09-078-294-12	Sequence 12, Appl
259	19	0.8	5208	4	US-09-618-166-70	Sequence 70, Appl	C 332	19	0.8	19011	1	US-08-310-356-36	Sequence 36, Appl
260	19	0.8	5275	1	US-08-485-588-1	Sequence 1, Appl	C 333	19	0.8	19557	5	PCT-US92-06300-1	Sequence 1, Appl
261	19	0.8	5275	1	US-08-494-565-1	Sequence 1, Appl	C 334	19	0.8	19736	4	US-09-740-035-3	Sequence 3, Appl
262	19	0.8	5275	2	US-08-480-751-1	Sequence 1, Appl	C 335	19	0.8	21234	4	US-09-810-671-3	Sequence 3, Appl
263	19	0.8	5275	2	US-08-943-866-1	Sequence 1, Appl	C 336	19	0.8	23187	4	US-09-499-522-1	Sequence 1, Appl
264	19	0.8	5275	3	US-08-353-784-1	Sequence 1, Appl	C 337	19	0.8	26016	4	US-09-326-480A-1	Sequence 1, Appl
265	19	0.8	5275	3	US-08-484-159B-1	Sequence 1, Appl	C 338	19	0.8	26664	4	US-09-564-805-28	Sequence 28, Appl
266	19	0.8	5275	4	US-08-484-159B-1	Sequence 1, Appl	C 339	19	0.8	28720	4	US-09-341-587-7	Sequence 7, Appl
267	19	0.8	5835	3	US-09-033-333-3	Sequence 3, Appl	C 340	19	0.8	29629	4	US-09-729-995-3	Sequence 3, Appl
268	19	0.8	5835	3	US-09-033-333-3	Sequence 3, Appl	C 341	19	0.8	31571	1	US-08-323-443B-1	Sequence 1, Appl
269	19	0.8	5835	4	US-09-033-556-2	Sequence 2, Appl	C 342	19	0.8	32654	4	US-09-801-191A-3	Sequence 3, Appl
270	19	0.8	5835	4	US-09-033-556-2	Sequence 2, Appl	C 343	19	0.8	35060	3	US-08-814-095-7	Sequence 7, Appl
271	19	0.8	5835	4	US-09-614-495-3	Sequence 3, Appl	C 344	19	0.8	35060	3	US-08-814-095-7	Sequence 7, Appl
272	19	0.8	5836	1	US-08-614-495-3	Sequence 3, Appl	C 345	19	0.8	35100	1	US-08-306-691B-19	Sequence 19, Appl
273	19	0.8	5836	1	US-08-380-916-1	Sequence 1, Appl	C 346	19	0.8	35100	5	PCT-US93-06251-19	Sequence 19, Appl
274	19	0.8	5836	1	US-08-380-916-1	Sequence 1, Appl	C 347	19	0.8	36159	4	US-09-749-588-3	Sequence 3, Appl
275	19	0.8	5836	3	US-08-721-690-1	Sequence 1, Appl	C 348	19	0.8	36159	4	US-09-749-588-3	Sequence 3, Appl
276	19	0.8	5836	3	US-08-721-690-1	Sequence 1, Appl	C 349	19	0.8	36741	3	US-09-301-665-3	Sequence 3, Appl
277	19	0.8	5836	3	US-08-891-581-1	Sequence 1, Appl	C 350	19	0.8	36741	3	US-09-301-665-3	Sequence 3, Appl
278	19	0.8	5836	3	US-08-891-581-1	Sequence 1, Appl	C 351	19	0.8	38653	4	US-09-922-445-1	Sequence 1, Appl
279	19	0.8	5836	3	US-09-033-333-2	Sequence 2, Appl	C 352	19	0.8	43069	4	US-09-292-542A-1	Sequence 1, Appl
280	19	0.8	5836	3	US-09-033-333-2	Sequence 2, Appl	C 353	19	0.8	43069	4	US-09-735-934A-3	Sequence 3, Appl
281	19	0.8	5836	4	US-09-033-556-1	Sequence 1, Appl	C 354	19	0.8	43950	4	US-09-735-934A-3	Sequence 3, Appl
282	19	0.8	5836	4	US-09-033-556-1	Sequence 1, Appl	C 355	19	0.8	43950	4	US-10-060-332-3	Sequence 3, Appl
283	19	0.8	5836	4	US-09-614-495-2	Sequence 2, Appl	C 356	19	0.8	43950	4	US-10-060-332-3	Sequence 3, Appl
284	19	0.8	5836	4	US-09-614-495-2	Sequence 2, Appl	C 357	19	0.8	44453	4	US-09-146-053-5	Sequence 5, Appl
285	19	0.8	5836	4	US-09-474-699-9	Sequence 9, Appl	C 358	19	0.8	45456	4	US-09-146-053-6	Sequence 6, Appl
286	19	0.8	5836	4	US-09-474-699-9	Sequence 9, Appl	C 359	19	0.8	45716	4	US-08-965-048-5	Sequence 5, Appl
287	19	0.8	5943	1	US-08-206-176-1	Sequence 1, Appl	C 360	19	0.8	45989	4	US-08-965-048-6	Sequence 6, Appl
288	19	0.8	6769	1	US-08-480-784-20	Sequence 20, Appl	C 361	19	0.8	50000	4	US-09-146-053-3	Sequence 3, Appl
289	19	0.8	6769	1	US-08-483-553-20	Sequence 20, Appl	C 362	19	0.8	50000	4	US-09-146-053-3	Sequence 3, Appl
290	19	0.8	6769	1	US-08-487-002-20	Sequence 20, Appl	C 363	19	0.8	50000	4	US-09-146-053-3	Sequence 3, Appl
291	19	0.8	6769	1	US-08-483-554B-20	Sequence 20, Appl	C 364	19	0.8	53332	4	US-09-801-861-3	Sequence 3, Appl
292	19	0.8	6769	1	US-08-488-011B-20	Sequence 20, Appl	C 365	19	0.8	53332	4	US-09-801-861-3	Sequence 3, Appl
293	19	0.8	6769	3	US-08-850-727-20	Sequence 20, Appl	C 366	19	0.8	53526	3	US-08-658-136-2	Sequence 2, Appl
294	19	0.8	6769	5	PCT-US95-10203-20	Sequence 20, Appl	C 367	19	0.8	53577	3	US-08-658-136-2	Sequence 2, Appl
295	19	0.8	6769	5	PCT-US95-10203-20	Sequence 20, Appl	C 368	19	0.8	55827	4	US-09-813-133A-3	Sequence 3, Appl
296	19	0.8	6769	5	PCT-US95-10203-20	Sequence 20, Appl	C 369	19	0.8	56516	2	US-08-996-306-1	Sequence 1, Appl
297	19	0.8	6799	4	US-09-620-312D-299	Sequence 299, App	C 370	19	0.8	56516	2	US-08-996-306-1	Sequence 1, Appl
298	19	0.8	7379	4	US-09-341-587-5	Sequence 5, Appl	C 371	19	0.8	56516	4	US-09-218-207-1	Sequence 1, Appl
299	19	0.8	8220	4	US-09-797-908-3	Sequence 3, Appl	C 372	19	0.8	56520	3	US-09-338-907-179	Sequence 179, App
300	19	0.8	8453	3	US-09-167-681-45	Sequence 45, Appl	C 373	19	0.8	56520	4	US-09-218-207-179	Sequence 179, App
301	19	0.8	9365	4	US-09-608-885A-8	Sequence 8, Appl	C 374	19	0.8	62804	4	US-09-800-960-3	Sequence 3, Appl
302	19	0.8	9365	4	US-09-350-836B-8	Sequence 8, Appl	C 375	19	0.8	70000	4	US-09-851-896-3	Sequence 3, Appl
303	19	0.8	9365	4	US-09-370-365-8	Sequence 8, Appl	C 376	19	0.8	72928	3	US-09-009-913-1	Sequence 1, Appl
304	19	0.8	9365	4	US-09-557-800C-8	Sequence 8, Appl	C 377	19	0.8	75395	4	US-09-984-890-3	Sequence 3, Appl
305	19	0.8	9371	4	US-09-801-874-3	Sequence 3, Appl	C 378	19	0.8	80246	3	US-09-078-294-4	Sequence 4, Appl
306	19	0.8	9721	3	US-09-345-172-2	Sequence 2, Appl	C 379	19	0.8	80595	3	US-09-078-294-3	Sequence 3, Appl
307	19	0.8	10504	4	US-09-423-744A-19	Sequence 19, Appl	C 380	19	0.8	83450	4	US-09-811-469-3	Sequence 3, Appl
308	19	0.8	10825	3	US-08-652-265-1	Sequence 1, Appl	C 381	19	0.8	84495	4	US-09-797-906-3	Sequence 3, Appl
309	19	0.8	10825	3	US-08-652-265-3	Sequence 3, Appl	C 382	19	0.8	87350	3	US-08-781-891-79	Sequence 79, Appl
310	19	0.8	10825	3	US-08-652-265-5	Sequence 5, Appl	C 383	19	0.8	87350	4	US-09-618-166-79	Sequence 79, Appl
311	19	0.8	10825	3	US-08-834-497A-1	Sequence 1, Appl	C 384	19	0.8	87543	4	US-09-791-211-3	Sequence 3, Appl
312	19	0.8	10825	3	US-08-834-497A-3	Sequence 3, Appl	C 385	19	0.8	90050	4	US-09-245-041-5	Sequence 5, Appl
313	19	0.8	10825	3	US-08-834-497A-5	Sequence 5, Appl	C 386	19	0.8	90541	4	US-09-759-359A-3	Sequence 3, Appl
314	19	0.8	10825	3	US-08-834-497A-7	Sequence 7, Appl	C 387	19	0.8	90541	4	US-09-759-359A-3	Sequence 3, Appl
315	19	0.8	10825	3	US-09-503-444A-1	Sequence 1, Appl	C 388	19	0.8	98844	4	US-09-791-211-10	Sequence 10, Appl
316	19	0.8	10825	3	US-09-503-444A-3	Sequence 3, Appl	C 389	19	0.8	99500	4	US-09-798-096-10	Sequence 10, Appl
317	19	0.8	10825	3	US-09-503-444A-5	Sequence 5, Appl	C 390	19	0.8	111282	4	US-09-754-250-3	Sequence 3, Appl
318	19	0.8	10825	3	US-09-503-444A-7	Sequence 7, Appl	C 391	19	0.8	111282	4	US-09-754-250-3	Sequence 3, Appl
319	19	0.8	10825	3	US-09-503-444A-7	Sequence 7, Appl	C 392	19	0.8	112132	4	US-09-741-150-3	Sequence 3, Appl

C 333	19	0.8	115592	4	US-09-818-512-3	Sequence 3, Appli	466	18	0.8	613	4	US-09-004-730A-47	Sequence 47, Appli
C 334	19	0.8	152331	3	US-09-128-155-16	Sequence 16, Appli	467	18	0.8	613	4	US-08-981-799A-47	Sequence 47, Appli
C 335	19	0.8	169998	4	US-09-676-610B-24	Sequence 24, Appli	C 469	18	0.8	617	3	US-09-385-882-222	Sequence 222, Appl
C 336	19	0.8	174493	4	US-09-804-471A-3	Sequence 3, Appli	469	18	0.8	629	2	US-08-698-805-3	Sequence 3, Appli
C 337	19	0.8	176373	3	US-09-128-155-17	Sequence 17, Appli	470	18	0.8	630	4	US-09-342-681C-5	Sequence 5, Appli
C 338	19	0.8	176496	4	US-09-877-177A-10	Sequence 10, Appli	C 471	18	0.8	642	3	US-09-288-143-35	Sequence 35, Appli
C 339	19	0.8	202001	4	US-09-734-674-3	Sequence 3, Appli	471	18	0.8	645	4	US-09-385-982-40	Sequence 40, Appli
C 400	19	0.8	319608	4	US-09-533-333D-1	Sequence 3, Appli	C 472	18	0.8	645	3	US-09-205-258-246	Sequence 246, Appl
C 401	19	0.8	319608	4	US-09-533-333D-1	Sequence 1, Appli	473	18	0.8	654	4	US-09-372-422A-45	Sequence 187, Appl
C 402	19	0.8	319608	4	US-09-533-333D-1	Sequence 1, Appli	474	18	0.8	678	4	US-09-328-475C-297	Sequence 189, Appl
C 403	19	0.8	319608	4	US-09-679-409-1	Sequence 1, Appli	475	18	0.8	681	4	US-09-328-475C-297	Sequence 237, Appl
C 404	19	0.8	319608	4	US-09-679-409-1	Sequence 1, Appli	476	18	0.8	686	4	US-08-466-047B-23	Sequence 236, Appl
C 405	19	0.8	1230025	4	US-09-138-452A-1	Sequence 1, Appli	C 477	18	0.8	733	3	US-08-936-165A-151	Sequence 23, Appli
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C 407	18	0.8	60	4	US-09-284-627-14	Sequence 14, Appli	C 480	18	0.8	752	4	US-09-374-678-7	Sequence 7, Appli
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C 410	18	0.8	135	2	US-08-799-464A-35	Sequence 35, Appli	481	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 411	18	0.8	171	2	US-08-799-464A-34	Sequence 34, Appli	482	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 412	18	0.8	235	2	US-08-849-701-9	Sequence 9, Appli	483	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 413	18	0.8	248	4	US-08-397-787-25	Sequence 25, Appli	C 484	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 414	18	0.8	300	4	US-09-205-258-143	Sequence 143, Appl	C 485	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 415	18	0.8	301	2	US-08-332-766A-23	Sequence 23, Appli	C 486	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 416	18	0.8	334	2	US-08-623-906A-9	Sequence 9, Appli	487	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 417	18	0.8	350	2	US-08-333-766A-20	Sequence 20, Appli	488	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 418	18	0.8	358	2	US-08-721-488-9	Sequence 9, Appli	489	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
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C 420	18	0.8	373	4	US-09-300-958A-15	Sequence 15, Appli	491	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 421	18	0.8	382	4	US-09-118-554A-59	Sequence 59, Appli	492	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 422	18	0.8	382	4	US-09-118-554A-59	Sequence 59, Appli	493	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
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C 426	18	0.8	433	1	US-08-117-080-13	Sequence 13, Appli	497	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
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C 432	18	0.8	472	3	US-09-357-141-55	Sequence 55, Appli	503	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 433	18	0.8	472	4	US-09-533-889-55	Sequence 55, Appli	504	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
C 434	18	0.8	472	4	US-09-702-705-892	Sequence 892, Appl	505	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
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C 437	18	0.8	472	4	US-09-679-299A-98	Sequence 98, Appli	508	18	0.8	773	3	US-08-906-769-80	Sequence 80, Appli
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740	18	0.8	3358	2	US-08-799-464A-1	Sequence 1, Appli	C 813	18	0.8	7676	1	US-08-451-777A-7	Sequence 7, Appli
741	18	0.8	3358	5	PCT-US95-09227-1	Sequence 1, Appli	C 814	18	0.8	7676	2	US-08-451-777A-7	Sequence 7, Appli
742	18	0.8	3387	1	US-08-064-271-11	Sequence 11, Appli	C 815	18	0.8	7676	2	US-08-998-208-7	Sequence 7, Appli
743	18	0.8	3387	2	US-08-627-254C-29	Sequence 29, Appli	C 816	18	0.8	7676	5	PCT-US95-06743-7	Sequence 7, Appli
744	18	0.8	3387	3	US-08-930-589A-19	Sequence 19, Appli	817	18	0.8	7941	4	US-09-816-703A-1	Sequence 1, Appli
745	18	0.8	3387	4	US-09-599-781-19	Sequence 19, Appli	C 818	18	0.8	8083	3	US-09-383-630-4	Sequence 4, Appli
746	18	0.8	3416	2	US-08-724-394A-15	Sequence 15, Appli	C 819	18	0.8	8083	3	US-09-383-630-5	Sequence 5, Appli
C 747	18	0.8	3694	4	US-09-232-200-46	Sequence 46, Appli	C 820	18	0.8	8992	3	US-08-976-255-5	Sequence 5, Appli
C 748	18	0.8	3694	4	US-09-232-197-46	Sequence 46, Appli	821	18	0.8	8992	3	US-08-458-434A-7	Sequence 68, Appli
C 749	18	0.8	3694	4	US-09-232-201-46	Sequence 46, Appli	822	18	0.8	9329	3	US-08-832-883-68	Sequence 68, Appli
C 750	18	0.8	3704	3	US-09-232-200-24	Sequence 24, Appli	823	18	0.8	9837	2	US-08-832-877-68	Sequence 68, Appli
C 751	18	0.8	3704	4	US-09-232-197-24	Sequence 24, Appli	824	18	0.8	9919	3	US-08-880-179-1	Sequence 1, Appli
C 752	18	0.8	3704	4	US-09-232-201-24	Sequence 24, Appli	825	18	0.8	10380	3	US-09-077-354B-3	Sequence 3, Appli
C 753	18	0.8	3742	1	US-08-694-915-5	Sequence 5, Appli	826	18	0.8	10640	4	US-09-417-485D-5	Sequence 5, Appli
C 754	18	0.8	3748	2	US-09-958-240-1	Sequence 1, Appli	827	18	0.8	10684	3	US-08-618-100B-3	Sequence 3, Appli
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756	18	0.8	3890	2	US-08-942-521B-1	Sequence 1, Appli	829	18	0.8	11721	4	US-09-026-039-3	Sequence 3, Appli
757	18	0.8	3890	3	US-09-192-702-1	Sequence 1, Appli	C 830	18	0.8	11721	4	US-09-026-039-3	Sequence 3, Appli

C 831	18	0.8	11789	4	US-09-387-286-57	Sequence 57, Appl	C 904	17	0.8	42	2	US-08-776-944-4	Sequence 4, Appl
C 832	18	0.8	11811	3	US-09-078-294-7	Sequence 7, Appl	C 905	17	0.8	45	1	US-08-522-623-6	Sequence 6, Appl
C 833	18	0.8	14042	3	US-08-552-877-85	Sequence 85, Appl	C 906	17	0.8	45	1	US-08-522-623-11	Sequence 11, Appl
C 834	18	0.8	14044	3	US-08-552-877-89	Sequence 89, Appl	C 907	17	0.8	45	5	US-08-522-623-6	Sequence 6, Appl
C 835	18	0.8	14080	3	US-08-552-877-87	Sequence 87, Appl	C 908	17	0.8	45	5	US-08-522-623-6	Sequence 11, Appl
C 836	18	0.8	14083	3	US-08-552-877-83	Sequence 83, Appl	C 909	17	0.8	47	3	US-09-338-907-275	Sequence 275, Appl
C 837	18	0.8	14086	3	US-08-552-877-83	Sequence 83, Appl	C 910	17	0.8	47	4	US-09-218-207-275	Sequence 275, Appl
C 838	18	0.8	14581	4	US-08-520-3730-4	Sequence 4, Appl	C 911	17	0.8	47	4	US-09-422-978-3455	Sequence 3455, Appl
C 839	18	0.8	15108	1	US-08-157-005-1	Sequence 1, Appl	C 912	17	0.8	48	2	US-08-563-368B-14	Sequence 14, Appl
C 840	18	0.8	15108	3	US-08-747-863-1	Sequence 1, Appl	C 913	17	0.8	48	2	US-08-563-368B-17	Sequence 17, Appl
C 841	18	0.8	15108	4	US-09-565-864-1	Sequence 1, Appl	C 914	17	0.8	51	2	US-08-101-751A-4	Sequence 4, Appl
C 842	18	0.8	15450	4	US-09-470-661A-1	Sequence 1, Appl	C 915	17	0.8	51	4	US-09-453-190B-3	Sequence 3, Appl
C 843	18	0.8	16595	4	US-09-146-053-7	Sequence 7, Appl	C 916	17	0.8	51	4	US-09-101-751A-17	Sequence 17, Appl
C 844	18	0.8	17606	3	US-08-943-731-4	Sequence 4, Appl	C 917	17	0.8	55	4	US-09-944-036-32	Sequence 32, Appl
C 845	18	0.8	18596	3	US-09-318-448-11	Sequence 11, Appl	C 918	17	0.8	56	4	US-09-944-036-30	Sequence 30, Appl
C 846	18	0.8	18597	4	US-09-362-665-8	Sequence 8, Appl	C 919	17	0.8	57	3	US-09-620-958A-7	Sequence 7, Appl
C 847	18	0.8	18853	4	US-09-820-005-3	Sequence 3, Appl	C 920	17	0.8	57	4	US-09-944-036-31	Sequence 31, Appl
C 848	18	0.8	20303	1	US-08-370-975B-6	Sequence 6, Appl	C 921	17	0.8	59	4	US-08-227-476-6	Sequence 6, Appl
C 849	18	0.8	21784	4	US-09-820-002-3	Sequence 3, Appl	C 922	17	0.8	67	3	US-09-620-958A-6	Sequence 6, Appl
C 850	18	0.8	24707	4	US-09-740-027-3	Sequence 3, Appl	C 923	17	0.8	68	3	US-08-118-200-7	Sequence 7, Appl
C 851	18	0.8	26754	1	US-08-370-975B-1	Sequence 1, Appl	C 924	17	0.8	68	3	US-08-458-745-7	Sequence 7, Appl
C 852	18	0.8	28994	3	US-08-884-324-14	Sequence 14, Appl	C 925	17	0.8	74	4	US-09-702-705-1592	Sequence 1592, Appl
C 853	18	0.8	28964	3	US-08-781-891-207	Sequence 207, Appl	C 926	17	0.8	74	4	US-09-736-457-1592	Sequence 1592, Appl
C 854	18	0.8	29604	4	US-09-618-166-207	Sequence 207, Appl	C 927	17	0.8	92	1	US-08-120-827-94	Sequence 94, Appl
C 855	18	0.8	37950	3	US-09-338-907-183	Sequence 183, Appl	C 928	17	0.8	92	1	US-08-478-675-94	Sequence 94, Appl
C 856	18	0.8	37950	4	US-09-218-207-183	Sequence 183, Appl	C 929	17	0.8	105	3	US-08-746-113-37	Sequence 37, Appl
C 857	18	0.8	38564	4	US-09-734-673-3	Sequence 3, Appl	C 930	17	0.8	109	1	US-08-120-827-84	Sequence 82, Appl
C 858	18	0.8	39882	4	US-09-820-024-3	Sequence 3, Appl	C 931	17	0.8	109	1	US-08-120-827-84	Sequence 84, Appl
C 859	18	0.8	40000	4	US-09-780-049-18	Sequence 18, Appl	C 932	17	0.8	109	1	US-08-478-675-82	Sequence 82, Appl
C 860	18	0.8	40328	4	US-08-742-185-102	Sequence 102, Appl	C 933	17	0.8	109	1	US-08-478-675-84	Sequence 84, Appl
C 861	18	0.8	40352	3	US-08-846-1110-15	Sequence 15, Appl	C 934	17	0.8	110	1	US-08-120-827-83	Sequence 83, Appl
C 862	18	0.8	40352	4	US-09-443-077-15	Sequence 15, Appl	C 935	17	0.8	110	1	US-08-478-675-83	Sequence 83, Appl
C 863	18	0.8	43795	3	US-08-742-185-101	Sequence 101, Appl	C 936	17	0.8	113	4	US-09-367-927A-1	Sequence 1, Appl
C 864	18	0.8	45546	4	US-09-146-053-6	Sequence 6, Appl	C 937	17	0.8	114	1	US-08-120-827-99	Sequence 99, Appl
C 865	18	0.8	48974	3	US-08-920-422-17	Sequence 17, Appl	C 938	17	0.8	114	1	US-08-478-675-99	Sequence 99, Appl
C 866	18	0.8	50000	4	US-09-146-053-4	Sequence 4, Appl	C 939	17	0.8	115	4	US-09-453-190B-9	Sequence 9, Appl
C 867	18	0.8	51552	4	US-09-733-294A-30	Sequence 30, Appl	C 940	17	0.8	120	1	US-08-153-051B-28	Sequence 28, Appl
C 868	18	0.8	59065	4	US-09-813-197-3	Sequence 3, Appl	C 941	17	0.8	120	1	US-08-060-952C-44	Sequence 44, Appl
C 869	18	0.8	59065	4	US-09-978-197-3	Sequence 3, Appl	C 942	17	0.8	120	2	US-08-151-477A-28	Sequence 28, Appl
C 870	18	0.8	63588	4	US-09-873-404-3	Sequence 3, Appl	C 943	17	0.8	120	3	US-08-819-867-58	Sequence 58, Appl
C 871	18	0.8	65042	4	US-09-784-316-3	Sequence 3, Appl	C 944	17	0.8	120	4	US-08-464-011B-44	Sequence 44, Appl
C 872	18	0.8	80246	3	US-09-078-294-4	Sequence 4, Appl	C 945	17	0.8	120	4	US-09-378-535-58	Sequence 58, Appl
C 873	18	0.8	80595	3	US-09-078-294-3	Sequence 3, Appl	C 946	17	0.8	139	3	US-09-084-120-18	Sequence 18, Appl
C 874	18	0.8	81001	4	US-09-750-580-1	Sequence 1, Appl	C 947	17	0.8	144	1	US-08-702-705-776	Sequence 26, Appl
C 875	18	0.8	87350	3	US-08-781-891-79	Sequence 79, Appl	C 948	17	0.8	144	4	US-09-702-705-776	Sequence 776, Appl
C 876	18	0.8	87350	4	US-09-618-166-79	Sequence 79, Appl	C 949	17	0.8	144	4	US-09-736-457-776	Sequence 776, Appl
C 877	18	0.8	87543	4	US-09-791-211-3	Sequence 3, Appl	C 950	17	0.8	189	3	US-08-481-190-7	Sequence 7, Appl
C 878	18	0.8	90050	3	US-09-245-041-5	Sequence 5, Appl	C 951	17	0.8	189	5	US-09-020-956-78	Sequence 78, Appl
C 879	18	0.8	148567	4	US-09-801-876B-3	Sequence 3, Appl	C 952	17	0.8	201	3	US-09-030-607-78	Sequence 78, Appl
C 880	18	0.8	152331	3	US-09-128-155-16	Sequence 16, Appl	C 953	17	0.8	201	3	US-09-439-313-78	Sequence 78, Appl
C 881	18	0.8	17493	4	US-09-804-471A-3	Sequence 3, Appl	C 954	17	0.8	201	4	US-09-352-616A-78	Sequence 78, Appl
C 882	18	0.8	176373	3	US-09-128-155-17	Sequence 17, Appl	C 955	17	0.8	201	4	US-09-232-149A-180	Sequence 180, Appl
C 883	18	0.8	1664976	4	US-08-516-421B-1	Sequence 1, Appl	C 956	17	0.8	215	3	US-08-751-359-23	Sequence 23, Appl
C 884	18	0.8	1830121	4	US-09-557-884-1	Sequence 1, Appl	C 957	17	0.8	215	4	US-08-907-146-23	Sequence 23, Appl
C 885	18	0.8	1830121	4	US-09-643-990A-1	Sequence 1, Appl	C 958	17	0.8	216	4	US-09-702-705-497	Sequence 497, Appl
C 886	17	0.8	19	4	US-09-475-947A-12	Sequence 12, Appl	C 959	17	0.8	216	4	US-09-736-457-497	Sequence 497, Appl
C 887	17	0.8	24	4	US-09-164-249B-6	Sequence 6, Appl	C 960	17	0.8	219	1	US-08-702-080-3	Sequence 3, Appl
C 888	17	0.8	30	2	US-08-629-001A-25	Sequence 25, Appl	C 961	17	0.8	219	2	US-08-858-830-3	Sequence 3, Appl
C 889	17	0.8	30	3	US-08-642-274D-104	Sequence 104, Appl	C 962	17	0.8	219	2	US-08-858-834-3	Sequence 3, Appl
C 890	17	0.8	32	3	US-09-368-991-1	Sequence 1, Appl	C 963	17	0.8	219	4	US-09-107-532A-3564	Sequence 3564, Appl
C 891	17	0.8	32	4	US-09-456-038-1	Sequence 1, Appl	C 964	17	0.8	222	3	US-08-481-190-15	Sequence 15, Appl
C 892	17	0.8	34	4	US-09-659-442-3	Sequence 3, Appl	C 965	17	0.8	222	5	US-09-792-594-11	Sequence 11, Appl
C 893	17	0.8	35	2	US-08-415-593-31	Sequence 31, Appl	C 966	17	0.8	223	4	US-09-397-787-129	Sequence 129, Appl
C 894	17	0.8	37	4	US-09-659-442-1	Sequence 1, Appl	C 967	17	0.8	228	4	US-08-222-177A-30	Sequence 30, Appl
C 895	17	0.8	37	4	US-09-659-442-2	Sequence 2, Appl	C 968	17	0.8	240	1	US-09-149-476-70	Sequence 70, Appl
C 896	17	0.8	40	2	US-08-415-593-46	Sequence 46, Appl	C 969	17	0.8	245	4	US-09-397-787-79	Sequence 79, Appl
C 897	17	0.8	40	3	US-08-688-514-13	Sequence 13, Appl	C 970	17	0.8	247	4	US-09-107-532A-3375	Sequence 3375, Appl
C 898	17	0.8	40	3	US-09-306-290-7	Sequence 7, Appl	C 971	17	0.8	249	4		
C 899	17	0.8	40	3	US-09-306-290-14	Sequence 14, Appl	C 972	17	0.8				
C 900	17	0.8	40	3	US-09-306-290-34	Sequence 34, Appl	C 973	17	0.8				
C 901	17	0.8	40	3	US-09-306-290-36	Sequence 36, Appl	C 974	17	0.8				
C 902	17	0.8	40	4	US-08-284-627-13	Sequence 13, Appl	C 975	17	0.8				
C 903	17	0.8	40	4	US-08-970-166-7	Sequence 7, Appl	C 976	17	0.8				

C 977 17 0.8 260 4 US-09-702-705-1208  
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986 17 0.8 297 4 US-09-305-839-17  
987 17 0.8 299 2 US-08-623-906A-19  
C 988 17 0.8 308 1 US-08-171-385-25  
C 989 17 0.8 308 3 US-08-361-441B-25  
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991 17 0.8 322 4 US-09-495-050A-281  
992 17 0.8 325 1 US-08-102-757-18  
993 17 0.8 334 2 US-08-522-421-3  
994 17 0.8 347 4 US-09-495-050A-188  
995 17 0.8 349 1 US-07-603-451A-4  
996 17 0.8 349 1 US-08-060-822A-4  
997 17 0.8 349 5 PCT-US94-05257-4  
998 17 0.8 350 1 US-08-248-016-11  
999 17 0.8 350 1 US-08-451-501-11  
1000 17 0.8 350 5 PCT-US95-06761-11

## ALIGNMENTS

RESULT 1  
US-08-861-549-2  
; Sequence 2, Application US/08861549  
; Patent No. 5874246  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Goli, Suriya K.  
; APPLICANT: Zhang, Hong  
; TITLE OF INVENTION: NEW TRANSCRIPTION REPRESSOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/861,549  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0306 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 737 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: SYNORAB01  
CLONE: 1620089

Sequence 1208, Ap  
Sequence 1208, Ap  
Sequence 27, Appl  
Sequence 159, App  
Sequence 3, Appli  
Sequence 1545, Ap  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 25, Appl  
Sequence 25, Appl  
Sequence 11, Appl  
Sequence 18, Appl  
Sequence 3, Appli  
Sequence 188, App  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 11, Appl

US-08-861-549-2

Query Match 1.2%; Score 27; DB 2; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2191 GAGGAGAGAGGTAGAGCTGTCTTAA 2217  
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Db 711 GAGGAGAGAGGTAGAGCTGTCTTAA 737

## RESULT 2

US-09-016-434-252  
; Sequence 252, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 252:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BRAITUT13  
CLONE: 1620089

US-09-016-434-252  
Query Match 1.2%; Score 27; DB 4; Length 738;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 712 GAGGAGAGAGGTAGAGCTGTCTTAA 738

## RESULT 3

US-09-920-759-13  
; Sequence 13, Application US/09920759  
; Patent No. 6537811  
; GENERAL INFORMATION:

APPLICANT: Brenda F. Baker  
APPLICANT: Susan M. Freier  
TITLE OF INVENTION: ANTISENSE MODULATION OF SAP-1 EXPRESSION  
FILE REFERENCE: RTS-0267  
CURRENT APPLICATION NUMBER: US/09/920,759  
CURRENT FILING DATE: 2001-08-01  
NUMBER OF SEQ ID NOS: 91  
SEQ ID NO 13  
LENGTH: 15788  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 690  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 691  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
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OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 711  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 712  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 713  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 714  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 715  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 716  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 717  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 718  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
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OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 720  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
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OTHER INFORMATION: unknown  
NAME/KEY: unsure  
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OTHER INFORMATION: unknown  
NAME/KEY: unsure  
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OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 724  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 725  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 726  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 727  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 728  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 729  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 730  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 731  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 732  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 733  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 734

; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 735  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 736  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 737  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 738  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 739  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 740  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 741  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 742  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 743  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 744  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 745  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 746  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 747  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 748  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 749  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 750  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 751

Query Match 1.1%; Score 24; DB 4; Length 15788;  
Best Local Similarity 100.0%; Pred.No. 0.71;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 CCAGCCTGGGTGACAGTGAGACTC 50  
Db 9784 CCAGCCTGGGTGACAGTGAGACTC 9807

## RESULT 4

US-09-780-049-18/c  
; Sequence 18, Application US/09780049  
; Patent No. 6465250  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT  
; FILE REFERENCE: RTS-0134  
; CURRENT APPLICATION NUMBER: US/09/780,049  
; CURRENT FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 96  
; SEQ ID NO 18  
; LENGTH: 40000  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-09-780-049-18

Query Match 1.1%; Score 24; DB 4; Length 40000;  
Best Local Similarity 100.0%; Pred.No. 0.66;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 CCAGCCTGGGTGACAGTGAGACTC 50  
Db 15461 CCAGCCTGGGTGACAGTGAGACTC 15438

## RESULT 5

US-09-345-882-1/c  
; Sequence 1, Application US/09345882  
; Patent No. 639373  
; GENERAL INFORMATION:  
; APPLICANT: Bouquellet, Lydie  
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7  
; FILE REFERENCE: GENSET-031A  
; CURRENT APPLICATION NUMBER: US/09/345,882  
; CURRENT FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: US 60/091,315  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/111,909  
; PRIOR FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1  
; LENGTH: 162450  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 72794  
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 88073  
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 90842  
; OTHER INFORMATION: 99-1437-335 : polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 93714  
; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 97122  
; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 97152  
; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 99098  
; OTHER INFORMATION: 5-130-257 : polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 99117  
; OTHER INFORMATION: 5-130-276 : polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 103806



[illegible]

OTHER INFORMATION: 5-131-395	:	polymorphic	base	A or T	FEATURE: NAME/KEY: allele LOCATION: 93690..93736 OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 106940	:	polymorphic	base	insertion of A	LOCATION: 93690..93736
OTHER INFORMATION: 5-133-375	:	polymorphic	base	insertion of A	OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 108106	:	polymorphic	base	insertion of A	LOCATION: 93690..93736
OTHER INFORMATION: 5-135-155	:	polymorphic	base	insertion of A	OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 108149	:	polymorphic	base	insertion of GTTT	LOCATION: 97099..97145
OTHER INFORMATION: 5-135-198	:	polymorphic	base	insertion of GTTT	OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 108308	:	polymorphic	base	A or G	LOCATION: 97099..97145
OTHER INFORMATION: 5-135-357	:	polymorphic	base	A or G	OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 108471	:	polymorphic	base	C or T	LOCATION: 97130..97177
OTHER INFORMATION: 5-136-174	:	polymorphic	base	C or T	OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 134134	:	polymorphic	base	C or T	LOCATION: 97130..97177
OTHER INFORMATION: 5-140-120	:	polymorphic	base	C or T	OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 134362	:	polymorphic	base	insertion of A	LOCATION: 99075..99121
OTHER INFORMATION: 5-140-348	:	polymorphic	base	insertion of A	OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 134374	:	polymorphic	base	insertion of CA	LOCATION: 99075..99121
OTHER INFORMATION: 5-140-361	:	polymorphic	base	insertion of CA	OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 146328	:	polymorphic	base	A or G	LOCATION: 99094..99140
OTHER INFORMATION: 5-143-84	:	polymorphic	base	A or G	OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 146345	:	polymorphic	base	A or C	LOCATION: 99094..99140
OTHER INFORMATION: 5-143-101	:	polymorphic	base	A or C	OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 150329	:	polymorphic	base	A or G	LOCATION: 103783..103828
OTHER INFORMATION: 5-145-24	:	polymorphic	base	A or G	OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 160031	:	polymorphic	base	G or T	LOCATION: 103783..103828
OTHER INFORMATION: 5-148-352	:	polymorphic	base	G or T	OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 72771..72817	:	polymorphic	fragment 5-124-273	SEQ ID30	LOCATION: 106918..106966
OTHER INFORMATION: 5-124-273	:	polymorphic	fragment 5-124-273	SEQ ID30	OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 72771..72817	:	polymorphic	fragment 5-124-273	SEQ ID51	LOCATION: 106918..106966
OTHER INFORMATION: 5-124-273	:	polymorphic	fragment 5-124-273	SEQ ID51	OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 88050..88096	:	polymorphic	fragment 5-127-261	SEQ ID31	LOCATION: 108084..108130
OTHER INFORMATION: 5-127-261	:	polymorphic	fragment 5-127-261	SEQ ID31	OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 88050..88096	:	polymorphic	fragment 5-127-261	SEQ ID52	LOCATION: 108084..108130
OTHER INFORMATION: 5-127-261	:	polymorphic	fragment 5-127-261	SEQ ID52	OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:	:				FEATURE:
NAME/KEY: allele	:				NAME/KEY: allele
LOCATION: 90819..90865	:	polymorphic	fragment 99-1437-325	SEQ ID49	LOCATION: 108127..108177
OTHER INFORMATION: 99-1437-325	:	polymorphic	fragment 99-1437-325	SEQ ID49	OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:	:				

Query Match 1.1%; Score 24; DB 4; Length 162450;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 CCAGCTGGTGACAGTGAATC 50  
|||||  
Db 54003 CCAGCTGGTGACAGTGAATC 53980

## RESULT 6

US-09-009-913-1/C  
; Sequence 1, Application US/09009913  
; Patent No. 6087485  
; GENERAL INFORMATION:  
; APPLICANT: Axys Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Asthma Related Genes  
; NUMBER OF SEQUENCES: 339  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bozicevic & Reed, LLP  
; STREET: 285 Hamilton Ave, Suite 200  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94301

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Fast-Seq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,913  
; FILING DATE: 21-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:

ATTORNEY/AGENT INFORMATION:  
; NAME: Sherwood, Pamela J  
; REGISTRATION NUMBER: 36,677  
; REFERENCE/DOCKET NUMBER: SEQ-4P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-327-3231  
; TELEFAX: 650-327-3231  
; TELEX:

INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 72928 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
US-09-009-913-1

Query Match 1.0%; Score 23; DB 3; Length 72928;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGTTGAAGTGACAGATCA 24  
|||||  
Db 47805 GAGGTTGAAGTGACAGATCA 47783

## RESULT 7

US-09-018-584A-27  
; Sequence 27, Application US/09018584A  
; Patent No. 623863  
; GENERAL INFORMATION:  
; APPLICANT: Schumm, James W.  
; APPLICANT: Bachter, Jeffery W.  
; TITLE OF INVENTION: MATERIALS AND METHODS FOR  
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM  
; REPEAT DNA MARKERS

NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Promega Corporation  
; STREET: 2800 Woods Hollow Road  
; CITY: Madison  
; STATE: Wisconsin  
; COUNTRY: U.S.A.  
; ZIP: 53711-5399  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb  
; COMPUTER: IBM compatible PC  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Word 97 (DOS text format)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/018,584A  
; FILING DATE: 04-Feb-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Grady J. Frenchick  
; REGISTRATION NUMBER: 29,018  
; REFERENCE/DOCKET NUMBER: 16026.9180  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (608) 257-3501  
; TELEFAX: (608) 257-2275

INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 333 bp  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Circular  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: no  
; IMMEDIATE SOURCE:  
; LIBRARY: plasmid, pGem3zf(+)  
; CLONE: G539  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: 15q26.2

US-09-018-584A-27

Query Match 1.0%; Score 22; DB 3; Length 333;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 AAAAAAGAAAGAAAAAGA 92  
|||||  
Db 58 AAAAAAGAAAGAAAAAGA 79

## RESULT 8

US-08-623-906A-17  
; Sequence 17, Application US/08623906A  
; Patent No. 5874217  
; GENERAL INFORMATION:  
; APPLICANT: Stevenson, Tamara  
; APPLICANT: Dvorak, Jan  
; APPLICANT: Halverson, Joy  
; TITLE OF INVENTION: Microsatellite Sequences for Canine  
; TITLE OF INVENTION: Genotyping  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALERITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94111-4187

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/623,906A

```
/
/
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sherwood, Pamela J.
/ REGISTRATION NUMBER: 36,677
/ REFERENCE/DOCKET NUMBER: A-62282/BIR
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-781-1989
/ TELEFAX: 415-398-3249
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 350 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..109
/ OTHER INFORMATION: /note= "Nucleotides 1-109 are
/ unique flanking sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 110..195
/ OTHER INFORMATION: /note= "Nucleotides 110-195 are
/ unique flanking sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 196..350
/ OTHER INFORMATION: /note= "Nucleotides 196-350 are
/ unique flanking sequence"
/
/ US-08-623-906A-17
/
/ Query Match 1.0%; Score 22; DB 2; Length 350;
/ Best Local Similarity 100.0%; Pred. No. 6.5;
/ Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 71 AAAAAAGAAAGAAAGAAAAAGA 92
/ 121 AAAAAAGAAAGAAAGAAAAAGA 142
/
/ Db
/
/ RESULT 9
/ US-08-646-301A-1
/ Sequence 1, Application US/08646301A
/ Patent No. 6194211
/ GENERAL INFORMATION:
/ APPLICANT: Richards, Cynthia Ann
/ TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
/ Antigen for Expression Targeting
/ FILE REFERENCE: PB1508USW
/ CURRENT APPLICATION NUMBER: US/08/646,301A
/ CURRENT FILING DATE: 1996-05-16
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 11288
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-08-646-301A-1
/
/ Query Match 1.0%; Score 22; DB 3; Length 11288;
/ Best Local Similarity 100.0%; Pred. No. 4.9;
/ Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 71 AAAAAAGAAAGAAAGAAAAAGA 92
/ 834 AAAAAAGAAAGAAAGAAAAAGA 855
/
/ Db
/
/ RESULT 10
/ US-08-481-968A-4
/ Sequence 4, Application US/08481968A
/ Patent No. 6300490
/ GENERAL INFORMATION:
/ APPLICANT: Huber, Brian
/ TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (CE
/ FILE REFERENCE: PB1087US4
/ CURRENT APPLICATION NUMBER: US/08/481,968A
/ CURRENT FILING DATE: 1998-06-07
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 11288
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-08-481-968A-4
/
/ Query Match 1.0%; Score 22; DB 4; Length 11288;
/ Best Local Similarity 100.0%; Pred. No. 4.9;
/ Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 71 AAAAAAGAAAGAAAGAAAAAGA 92
/ 834 AAAAAAGAAAGAAAGAAAAAGA 855
/
/ Db
/
/ RESULT 11
/ US-08-154-712B-4
/ Sequence 4, Application US/08154712B
/ Patent No. 6337209
/ GENERAL INFORMATION:
/ APPLICANT: Huber, Brian
/ TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen Rec
/ FILE REFERENCE: PB1087US3
/ CURRENT APPLICATION NUMBER: US/08/154,712B
/ CURRENT FILING DATE: 1993-11-19
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 11288
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-08-154-712B-4
/
/ Query Match 1.0%; Score 22; DB 4; Length 11288;
/ Best Local Similarity 100.0%; Pred. No. 4.9;
/ Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 71 AAAAAAGAAAGAAAGAAAAAGA 92
/ 834 AAAAAAGAAAGAAAGAAAAAGA 855
/
/ Db
/
/ RESULT 12
/ US-09-474-699-10
/ Sequence 10, Application US/09474699
/ Patent No. 6495130
/ GENERAL INFORMATION:
/ APPLICANT: Henderson, Daniel R.
/ TITLE OF INVENTION: TARGET CELL-SPECIFIC ADENOVIRAL VECTORS
/ FILE REFERENCE: 348022001300
/ CURRENT APPLICATION NUMBER: US/09/474,699
/ CURRENT FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 60/114,262
/ PRIOR FILING DATE: 1998-12-30
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 10
; LENGTH: 15056
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-474-699-10
Query Match      1.0%; Score 22; DB 4; Length 15056;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 71 AAAAAAGAAAGAAAGAAAGAAAGA 92
Db 4602 AAAAAAGAAAGAAAGAAAGAAAGA 4623

RESULT 13
US-09-738-894A-3
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3
Query Match      1.0%; Score 22; DB 4; Length 36651;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 71 AAAAAAGAAAGAAAGAAAGAAAGA 92
Db 5334 AAAAAAGAAAGAAAGAAAGAAAGA 5355

RESULT 14
US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636Div
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3
Query Match      1.0%; Score 22; DB 4; Length 36651;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Patent No. 6528268
; GENERAL INFORMATION:
; APPLICANT: Andersson, Maria K.
; APPLICANT: Berglund, Lars G. T.
; APPLICANT: Reneland, Rikard H.
; APPLICANT: Adam, Gail I. R.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
; FILE REFERENCE: GG126US
; CURRENT APPLICATION NUMBER: US/09/922,445
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 51
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; ORGANISM: homo sapiens
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)

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Title: US-09-667-170A-440

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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18	415	18.5	520	14	US-10-163-866-32	Sequence 32, Appl
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20	281	12.6	337	10	US-09-854-133-442	Sequence 442, App
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c 142	23	1.0	747	13	US-10-027-632-144503	Sequence 144503, A	c 215	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 143	23	1.0	748	13	US-10-027-632-8530	Sequence 8530, Ap	c 216	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 144	23	1.0	753	14	US-10-106-698-720	Sequence 720, App	c 217	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 145	23	1.0	802	13	US-10-027-632-140720	Sequence 140720, A	c 218	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 146	23	1.0	810	13	US-10-027-632-169650	Sequence 169650, A	c 219	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 147	23	1.0	832	14	US-10-198-846-6585	Sequence 6585, Ap	c 220	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 148	23	1.0	900	13	US-10-027-632-173214	Sequence 173214, A	c 221	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 149	23	1.0	906	13	US-10-027-632-173215	Sequence 173215, A	c 222	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 150	23	1.0	950	13	US-10-027-632-129934	Sequence 129934, A	c 223	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 151	23	1.0	1118	10	US-09-764-877-2777	Sequence 2777, Ap	c 224	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 152	23	1.0	1815	11	US-09-822-846-60	Sequence 846, A	c 225	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 153	23	1.0	2051	14	US-10-198-846-11396	Sequence 11396, A	c 226	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 154	23	1.0	2361	9	US-09-925-302-281	Sequence 302, A	c 227	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 155	23	1.0	2848	13	US-10-027-632-112062	Sequence 112062, A	c 228	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 156	23	1.0	3109	11	US-09-746-783-85	Sequence 783, A	c 229	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 157	23	1.0	4342	12	US-10-017-161-821	Sequence 85, Appl	c 230	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 158	23	1.0	5958	12	US-10-311-455-1032	Sequence 821, App	c 231	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 159	23	1.0	7386	10	US-09-764-855-208	Sequence 208, App	c 232	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 160	23	1.0	7386	14	US-10-072-349-208	Sequence 208, App	c 233	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 161	23	1.0	10020	12	US-10-311-455-2265	Sequence 2265, Ap	c 234	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap
c 162	23	1.0	17216	10	US-09-764-877-3565	Sequence 3565, Ap	c 235	22	1.0	613	14	US-10-198-846-7691	Sequence 7691, Ap

C 236	22	1.0	827	13	US-10-027-632-161941	Sequence 161941,	C 309	22	1.0	22645	11	US-09-764-891-7673	Sequence 7673, Ap
237	22	1.0	879	13	US-10-027-632-101288	Sequence 101288,	C 310	22	1.0	22645	11	US-09-764-891-8183	Sequence 8183, Ap
238	22	1.0	879	13	US-10-027-632-101289	Sequence 101289,	C 311	22	1.0	25277	9	US-09-764-878-285	Sequence 285, Ap
239	22	1.0	1041	13	US-10-027-632-116643	Sequence 116643,	C 312	22	1.0	25277	9	US-09-764-860-1148	Sequence 1148, Ap
240	22	1.0	1041	13	US-10-027-632-116644	Sequence 116644,	C 313	22	1.0	25277	14	US-10-079-854-285	Sequence 285, Ap
241	22	1.0	1041	13	US-10-027-632-116645	Sequence 116645,	C 314	22	1.0	25277	14	US-10-074-095-1148	Sequence 1148, Ap
242	22	1.0	1042	13	US-10-027-632-116648	Sequence 116648,	C 315	22	1.0	25279	9	US-09-764-878-284	Sequence 284, Ap
243	22	1.0	1072	13	US-10-027-632-116539	Sequence 116539,	C 316	22	1.0	25279	9	US-09-764-860-1147	Sequence 1147, Ap
244	22	1.0	1072	13	US-10-027-632-116540	Sequence 116540,	C 317	22	1.0	25279	14	US-10-079-854-284	Sequence 284, Ap
245	22	1.0	1072	13	US-10-027-632-116541	Sequence 116541,	C 318	22	1.0	25279	14	US-10-074-095-1147	Sequence 1147, Ap
246	22	1.0	1128	13	US-10-027-632-31730	Sequence 31730, A	C 319	22	1.0	27062	11	US-09-764-891-8034	Sequence 8034, Ap
C 247	22	1.0	1131	13	US-10-027-632-264581	Sequence 264581,	C 320	22	1.0	31168	10	US-09-764-868-1464	Sequence 1464, Ap
C 248	22	1.0	1131	13	US-10-027-632-264582	Sequence 264582,	C 321	22	1.0	31994	9	US-09-764-860-599	Sequence 599, Ap
C 249	22	1.0	1475	12	US-10-261-078-3	Sequence 3, Appli	C 322	22	1.0	31994	10	US-09-764-904-71	Sequence 71, Appl
C 250	22	1.0	1556	13	US-10-027-632-256224	Sequence 256224, A	C 323	22	1.0	31994	14	US-10-091-548-71	Sequence 71, Appl
C 251	22	1.0	1816	13	US-10-027-632-51324	Sequence 51324, A	C 324	22	1.0	31994	14	US-10-071-095-599	Sequence 599, Ap
C 252	22	1.0	1816	13	US-10-027-632-51325	Sequence 51325, A	C 325	22	1.0	32193	14	US-09-764-877-2147	Sequence 2147, Ap
C 253	22	1.0	1816	13	US-10-027-632-51326	Sequence 51326, A	C 326	22	1.0	32193	11	US-09-764-891-7028	Sequence 7028, Ap
C 254	22	1.0	2288	13	US-10-027-632-51327	Sequence 51327, A	C 327	22	1.0	36651	9	US-09-964-469-3	Sequence 3, Appli
C 255	22	1.0	2288	13	US-10-027-632-102001	Sequence 102001,	C 328	22	1.0	36651	12	US-10-425-962-3	Sequence 3, Appli
C 256	22	1.0	2325	13	US-10-027-632-103528	Sequence 103528,	C 329	22	1.0	41104	9	US-09-816-685-3	Sequence 3, Appli
C 257	22	1.0	2325	13	US-10-027-632-103529	Sequence 103529,	C 330	22	1.0	42863	12	US-10-017-161-1017	Sequence 1017, Ap
C 258	22	1.0	2384	13	US-10-027-632-111547	Sequence 111547,	C 331	22	1.0	46130	12	US-10-017-161-985	Sequence 985, Ap
C 259	22	1.0	2754	10	US-09-880-107-3720	Sequence 3720, Ap	C 332	22	1.0	50000	14	US-10-152-724A-21	Sequence 21, Appl
C 260	22	1.0	2921	14	US-10-198-846-11998	Sequence 11998, A	C 333	22	1.0	55611	12	US-10-017-161-783	Sequence 783, Ap
C 261	22	1.0	3233	12	US-09-964-824A-116	Sequence 116, Ap	C 334	22	1.0	63000	10	US-09-780-172-18	Sequence 18, Appl
C 262	22	1.0	3233	12	US-09-873-319-301	Sequence 301, Ap	C 335	22	1.0	64467	14	US-10-274-409-3	Sequence 3, Appli
C 263	22	1.0	3233	12	US-09-960-706-494	Sequence 494, Ap	C 336	22	1.0	65464	10	US-09-858-888-3	Sequence 3, Appli
C 264	22	1.0	3303	13	US-10-027-632-115241	Sequence 115241,	C 337	22	1.0	88191	10	US-09-799-799-3	Sequence 3, Appli
C 265	22	1.0	3303	13	US-10-027-632-115242	Sequence 115242,	C 338	22	1.0	89094	10	US-09-880-107-3428	Sequence 3428, Ap
C 266	22	1.0	3593	14	US-10-002-775-10	Sequence 10, Appl	C 339	22	1.0	113000	12	US-10-376-566-16	Sequence 16, Appl
C 267	22	1.0	3593	14	US-10-115-615-22	Sequence 22, Appl	C 340	22	1.0	113604	14	US-10-227-195A-1	Sequence 1, Appli
C 268	22	1.0	4203	11	US-09-764-891-7948	Sequence 7948, Ap	C 341	22	1.0	113604	14	US-10-227-195A-2	Sequence 2, Appli
C 269	22	1.0	4369	11	US-09-764-877-2824	Sequence 2824, Ap	C 342	22	1.0	118652	15	US-10-081-327-32	Sequence 32, Appl
270	22	1.0	5281	11	US-09-764-891-6949	Sequence 6949, Ap	C 343	22	1.0	161652	15	US-10-081-327-40	Sequence 40, Appl
271	22	1.0	5314	12	US-10-311-455-134	Sequence 134, Ap	C 344	22	1.0	167343	10	US-09-962-436-281	Sequence 281, Ap
272	22	1.0	5314	12	US-10-240-452-10	Sequence 10, Appl	C 345	22	1.0	170834	9	US-09-964-824A-273	Sequence 273, Ap
273	22	1.0	5586	12	US-10-311-455-621	Sequence 621, Ap	C 346	22	1.0	170834	12	US-09-835-232-7	Sequence 7, Appli
274	22	1.0	5744	14	US-09-764-847-1457	Sequence 1457, Ap	C 347	22	1.0	170834	12	US-10-308-485-7	Sequence 7, Appli
275	22	1.0	5744	14	US-10-092-154-1457	Sequence 1457, Ap	C 348	22	1.0	235033	14	US-10-301-844-1	Sequence 1, Appli
C 276	22	1.0	5986	12	US-10-311-455-2068	Sequence 2068, Ap	C 349	22	1.0	237326	14	US-10-301-844-2	Sequence 2, Appli
C 277	22	1.0	6012	12	US-10-240-453-211	Sequence 211, Ap	C 350	22	1.0	250000	12	US-10-225-810-26	Sequence 26, Appl
278	22	1.0	6020	12	US-10-204-708-8	Sequence 8, Appli	C 351	22	1.0	254366	11	US-09-822-871-3	Sequence 3, Appli
279	22	1.0	6020	12	US-10-311-455-172	Sequence 172, Ap	C 352	22	1.0	300000	14	US-10-262-552-33	Sequence 33, Appl
280	22	1.0	6103	12	US-10-311-455-2144	Sequence 2144, Ap	C 353	22	1.0	684973	10	US-09-263-959-1	Sequence 1, Appli
281	22	1.0	6195	12	US-10-311-455-564	Sequence 564, Ap	C 354	22	1.0	1503841	9	US-09-795-668-1	Sequence 1, Appli
282	22	1.0	8404	12	US-10-311-455-1567	Sequence 1567, Ap	C 355	22	1.0	1503841	9	US-09-795-668-1	Sequence 1, Appli
283	22	1.0	8677	10	US-09-764-877-3322	Sequence 3322, Ap	C 356	22	1.0	1503841	9	US-09-795-686-1	Sequence 1, Appli
284	22	1.0	8680	10	US-09-764-877-3321	Sequence 3321, Ap	C 357	22	1.0	1503841	9	US-09-795-686-1	Sequence 1, Appli
C 285	22	1.0	8866	12	US-10-240-453-154	Sequence 154, Ap	C 358	22	1.0	1503841	10	US-09-946-807-1	Sequence 1, Appli
C 286	22	1.0	8866	14	US-10-239-676-140	Sequence 140, Ap	C 359	22	1.0	1503841	10	US-09-946-807-1	Sequence 1, Appli
C 287	22	1.0	8962	12	US-10-311-455-660	Sequence 660, Ap	C 360	22	1.0	2940917	13	US-10-027-632-174763	Sequence 174763,
C 288	22	1.0	9372	10	US-09-764-877-3049	Sequence 3049, Ap	C 361	21	0.9	241	10	US-09-833-381-1089	Sequence 1089, Ap
C 289	22	1.0	9372	10	US-09-764-877-3244	Sequence 3244, Ap	C 362	21	0.9	273	11	US-09-764-891-7564	Sequence 7564, Ap
C 290	22	1.0	9723	12	US-10-311-455-2354	Sequence 2354, Ap	C 363	21	0.9	276	11	US-09-764-891-7561	Sequence 7561, Ap
C 291	22	1.0	9927	12	US-10-311-455-85	Sequence 85, Appl	C 364	21	0.9	283	10	US-09-917-800A-460	Sequence 460, Ap
292	22	1.0	10429	9	US-09-764-891-7375	Sequence 7375, Ap	C 365	21	0.9	284	12	US-09-814-353-17553	Sequence 17553, A
293	22	1.0	11288	11	US-09-947-925A-4	Sequence 4, Appli	C 366	21	0.9	326	12	US-09-814-353-18362	Sequence 18362, A
294	22	1.0	11288	10	US-09-822-634-1	Sequence 1, Appli	C 367	21	0.9	329	12	US-09-814-353-2705	Sequence 2705, Ap
C 295	22	1.0	11838	11	US-09-764-891-7020	Sequence 7020, Ap	C 368	21	0.9	329	12	US-09-814-353-9038	Sequence 9038, Ap
C 296	22	1.0	14410	11	US-09-764-891-8697	Sequence 8697, Ap	C 369	21	0.9	341	11	US-09-918-995-19067	Sequence 19067, A
C 297	22	1.0	14874	11	US-09-764-891-7672	Sequence 7672, Ap	C 370	21	0.9	349	12	US-09-814-353-18039	Sequence 18039, A
C 298	22	1.0	15002	11	US-09-770-107-3	Sequence 3, Appli	C 371	21	0.9	351	12	US-09-814-353-17579	Sequence 17579, A
C 299	22	1.0	15056	9	US-09-392-822-4	Sequence 4, Appli	C 372	21	0.9	353	11	US-09-918-995-17718	Sequence 17718, A
300	22	1.0	15056	11	US-09-814-357-14	Sequence 14, Appl	C 373	21	0.9	355	11	US-09-803-719-442	Sequence 442, Ap
301	22	1.0	15056	12	US-09-814-351-14	Sequence 14, Appl	C 374	21	0.9	376	9	US-09-770-791-249	Sequence 249, Ap
302	22	1.0	15056	14	US-10-045-116-25	Sequence 25, Appl	C 375	21	0.9	396	13	US-10-027-632-143615	Sequence 143615,
303	22	1.0	15056	14	US-10-226-820-10	Sequence 10, Appl	C 376	21	0.9	403	12	US-09-814-353-17949	Sequence 17949, A
C 304	22	1.0	16579	11	US-09-764-891-8443	Sequence 8443, Ap	C 377	21	0.9	405	11	US-09-918-995-37246	Sequence 37246, A
C 305	22	1.0	17252	9	US-09-764-860-1102	Sequence 1102, Ap	C 378	21	0.9	413	11	US-09-918-995-17359	Sequence 17359, A
C 306	22	1.0	17252	14	US-10-074-095-1102	Sequence 1102, Ap	C 379	21	0.9	424	11	US-09-918-995-16049	Sequence 16049, A
C 307	22	1.0	17993	10	US-09-768-781-5	Sequence 5, Appli	C 380	21	0.9	425	11	US-09-918-995-23485	Sequence 23485, A
C 308	22	1.0	22609	10	US-09-764-877-2146	Sequence 2146, Ap	C 381	21	0.9	427	11	US-09-918-995-17115	Sequence 17115, A



C 382	21	0.9	430	11	US-09-918-995-34700	Sequence 34700, A	455	21	0.9	539	14	US-10-313-542-236	Sequence 236, App
C 383	21	0.9	430	11	US-09-918-995-34846	Sequence 34846, A	456	21	0.9	611	13	US-10-027-632-204567	Sequence 204567, App
C 384	21	0.9	451	9	US-09-864-761-5293	Sequence 5293, Ap	457	21	0.9	613	13	US-10-027-632-214800	Sequence 214800, App
C 385	21	0.9	463	13	US-10-027-632-282957	Sequence 282957, A	458	21	0.9	617	13	US-10-027-632-122200	Sequence 122200, App
C 386	21	0.9	466	13	US-10-027-632-89647	Sequence 89647, A	459	21	0.9	618	13	US-10-027-632-96765	Sequence 96765, A
C 387	21	0.9	466	13	US-10-027-632-17215	Sequence 17215, A	460	21	0.9	618	13	US-10-027-632-267651	Sequence 267651, A
C 388	21	0.9	466	14	US-10-060-036-2357	Sequence 2357, Ap	461	21	0.9	618	13	US-10-027-632-308357	Sequence 308357, App
C 389	21	0.9	472	11	US-09-918-995-12888	Sequence 12888, A	462	21	0.9	624	13	US-10-027-632-238994	Sequence 238994, App
C 390	21	0.9	473	12	US-09-814-353-15422	Sequence 15422, A	463	21	0.9	624	13	US-10-027-632-238995	Sequence 238995, App
C 391	21	0.9	476	11	US-09-918-995-20128	Sequence 20128, A	464	21	0.9	624	13	US-10-027-632-245434	Sequence 245434, App
C 392	21	0.9	482	13	US-10-027-632-114819	Sequence 114819, A	465	21	0.9	624	13	US-10-027-632-252776	Sequence 252776, App
C 393	21	0.9	482	13	US-10-027-632-114820	Sequence 114820, A	466	21	0.9	626	13	US-10-027-632-80782	Sequence 80782, A
C 394	21	0.9	486	13	US-10-027-632-135134	Sequence 135134, A	467	21	0.9	632	13	US-10-027-632-277571	Sequence 277571, App
C 395	21	0.9	488	11	US-09-918-995-4788	Sequence 4788, Ap	468	21	0.9	634	13	US-10-027-632-290545	Sequence 290545, App
C 396	21	0.9	495	13	US-10-027-632-183036	Sequence 183036, A	469	21	0.9	630	13	US-10-027-632-185104	Sequence 185104, App
C 397	21	0.9	499	13	US-10-027-632-105984	Sequence 105984, A	470	21	0.9	658	13	US-10-027-632-221216	Sequence 221216, App
C 398	21	0.9	499	13	US-10-027-632-127943	Sequence 127943, A	471	21	0.9	650	13	US-10-027-632-221217	Sequence 221217, App
C 399	21	0.9	505	13	US-10-027-632-81848	Sequence 81848, A	472	21	0.9	656	13	US-10-027-632-275991	Sequence 275991, App
C 400	21	0.9	505	13	US-10-027-632-292802	Sequence 292802, A	473	21	0.9	657	13	US-10-027-632-275990	Sequence 275990, App
C 401	21	0.9	506	11	US-09-770-961-295	Sequence 295, App	474	21	0.9	667	13	US-10-027-632-201563	Sequence 201563, App
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C 405	21	0.9	520	13	US-10-027-632-59434	Sequence 59434, A	478	21	0.9	673	14	US-10-106-698-1535	Sequence 1535, Ap
C 406	21	0.9	520	13	US-10-027-632-59435	Sequence 59435, A	479	21	0.9	689	13	US-10-027-632-18784	Sequence 18784, A
C 407	21	0.9	534	13	US-10-027-632-62213	Sequence 62213, A	480	21	0.9	697	13	US-10-027-632-18506	Sequence 18506, A
C 408	21	0.9	534	13	US-10-027-632-63102	Sequence 63102, A	481	21	0.9	697	13	US-10-027-632-38495	Sequence 38495, A
C 409	21	0.9	536	13	US-10-027-632-36732	Sequence 36732, A	482	21	0.9	716	13	US-10-027-632-18945	Sequence 18945, A
C 410	21	0.9	536	13	US-10-027-632-36733	Sequence 36733, A	483	21	0.9	721	13	US-10-027-632-189161	Sequence 189161, App
C 411	21	0.9	539	13	US-10-027-632-37664	Sequence 37664, A	484	21	0.9	721	13	US-10-027-632-149162	Sequence 149162, App
C 412	21	0.9	539	13	US-10-027-632-11677	Sequence 11677, A	485	21	0.9	724	13	US-10-027-632-138318	Sequence 138318, App
C 413	21	0.9	539	13	US-10-027-632-112678	Sequence 112678, A	486	21	0.9	728	13	US-10-027-632-113907	Sequence 113907, App
C 414	21	0.9	539	13	US-10-027-632-306523	Sequence 306523, A	487	21	0.9	728	13	US-10-027-632-19831	Sequence 19831, A
C 415	21	0.9	546	13	US-10-027-632-5004	Sequence 5004, Ap	488	21	0.9	728	13	US-10-027-632-127549	Sequence 127549, App
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C 417	21	0.9	547	13	US-10-027-632-47318	Sequence 47318, A	490	21	0.9	731	13	US-10-027-632-18111	Sequence 18111, A
C 418	21	0.9	549	13	US-10-027-632-254297	Sequence 254297, A	491	21	0.9	731	13	US-10-027-632-151734	Sequence 151734, App
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C 425	21	0.9	555	13	US-10-027-632-316641	Sequence 316641, A	498	21	0.9	769	13	US-10-027-632-158697	Sequence 158697, App
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Db 1861 TTTCATATATTTTACGATATTCGAACCTAAATTTCTAAGAAAAATTTAGTTTAACTCTATCTAG 1920  
Qy 1921 TTATAGAAAGTGAATATGCAAGTTATTTCTATGAGTGGCACAATTTCTTGAGTCTCTGATACC 1980  
Db 1921 TTATAGAAAGTGAATATGCAAGTTATTTCTATGAGTGGCACAATTTCTTGAGTCTCTGATACC 1980  
Qy 1981 TACCTATTGGGGTTAGGAGAAAAAGACTTAGACAATTTACTATGAGTGGCACAATTTCTTGAGTCTCTGATACC 2040  
Db 1981 TACCTATTGGGGTTAGGAGAAAAAGACTTAGACAATTTACTATGAGTGGCACAATTTCTTGAGTCTCTGATACC 2040  
Qy 2041 ATGTTAGCACGGCAAAAGAACCTTTCAAATTTGAGACTGAGATTTTCTGTATATATGAGTT 2100  
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Db 2161 AAAAAAGACATACATCATGATTTATGCAAGAGAGAGAGAGAGTGTTCATTTCTG 2220  
Qy 2221 TATTTAAAAAATAAAAAA 2239  
Db 2221 TATTTAAAAAATAAAAAA 2239

## RESULT 3

US-10-144-649A-440  
; Sequence 440, Application US/10144649A  
; Publication No. US20030118599A1  
; GENERAL INFORMATION:  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Pan, Liqueun  
; APPLICANT: Algate, Paul A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: 210121.475C11  
; CURRENT APPLICATION NUMBER: US/10/144,649A  
; CURRENT FILING DATE: 2002-08-21  
; NUMBER OF SEQ ID NOS: 749  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 440  
; LENGTH: 2239  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-144-649A-440

Query Match 100.0%; Score 2239; DB 14; Length 2239;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGTTGAAGTGAAGAGAGATCATCCAGCTGGGTGACAGTGTCTGTCTCAAC 60  
Db 1 GGAGGTTGAAGTGAAGAGAGATCATCCAGCTGGGTGACAGTGTCTGTCTCAAC 60







Db 2221 TATTAAAAA 2239

RESULT 4

US-09-738-973-441

; Sequence 441, Application US/09738973

; Patent No. US20020110563A1

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Fling, Steven P.

; APPLICANT: Mohamath, Raodoh

; APPLICANT: Algate, Paul A.

; APPLICANT: Secrist, Heather

; APPLICANT: Indrias, Carol Yoseph

; APPLICANT: Benson, Darin R.

; APPLICANT: Elliot, Mark

; APPLICANT: Mannion, Jane

; APPLICANT: Kalos, Michael D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; FILE REFERENCE: 210121.475C9

; CURRENT APPLICATION NUMBER: US/09/738,973

; CURRENT FILING DATE: 2000-12-14

; NUMBER OF SEQ ID NOS: 587

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 441

; LENGTH: 5981

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-738-973-441

Query Match 83.4%; Score 1867; DB 10; Length 5981;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 GAGAAAGTGCAGTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCAATTGGC 393

Db 278 GAGAAAGTGCAGTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCAATTGGC 337

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Db 338 ACCATCATGGAGGAGGAATCTTCATCTCTCTAAGGGGCTGCTCCAGAACACGGGACG 397

QY 454 GTGGGCACTGCTCTGACCATCTGGAGGAGTGTGGGGTCTGTGCTATTTGGAGCTTTG 513

Db 398 GTGGGCACTGCTCTGACCATCTGGAGGAGTGTGGGGTCTGTGCTATTTGGAGCTTTG 457

QY 514 TCTTATGCTGAATTTGGGAACAACTATAAGAAATCTGGAGGTCATTACACATATATTTG 573

Db 458 TCTTATGCTGAATTTGGGAACAACTATAAGAAATCTGGAGGTCATTACACATATATTTG 517

QY 574 GAAGTCTTTGGTCCATTACAGCTTTTGTACAGTCTGGGTGGAACTCCTCATATACGC 633

Db 518 GAAGTCTTTGGTCCATTACAGCTTTTGTACAGTCTGGGTGGAACTCCTCATATACGC 577

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QY 694 ATTCAATCTGAATCCCTGAACTTCGGATCAAGCTCATTACAGCTGTGGGCATTAACCTGA 753

Db 638 ATTCAATCTGAATCCCTGAACTTCGGATCAAGCTCATTACAGCTGTGGGCATTAACCTGA 697

QY 754 GTGATGCTCTTAATPAGCATGAGTGTACGTGGAGCGCCGGATCCAGATTTCTTAACC 813

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Db 1358 AGTGGCTTTTATTATGGGCTGGCAGTGTGCTGGGCTGATTTATCTTCGATACAAATGCCCA 1417

QY 1474 GATATGATCTGCTCTTCAAGGTGCCACTGTTCATCCAGCTTTGTTTCTTCCATCAGTGC 1533

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Db 1658 CCAGAGAGATAGTATGAACTAATPGACTTGGACATTTGGCAATCTCCGCCAAGGGGA 1717

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Db 1718 GACACAAATAGGGATTTTACTTTTCAATTTTATTCATATTTTATGCAATTTTCTTGGTG 1777

QY 1834 ATAAACAAAGAGTCAAGTTATTTTATTCATATTTTATGCAATTTTCTGAACTAATTTCT 1893

Db 1778 ATAAACAAAGAGTCAAGTTATTTTATTCATATTTTATGCAATTTTCTGAACTAATTTCT 1837

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QY 1954 TCSCACAATTTCTGAGTCTCTGATCTACCTATTATGGGGTTAGGAGAAAGATAGACAA 2013

Db 1898 TCGCAAAATCTTGAGTCTCTCATACCTACCTATTGGGTTAGGAGAAAGACTAGACAA 1957  
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Qy 2074 ACTGAGATTTTCTGTATATATGTTGTTTGTAAAGATGTTTACACATACAGATGCT 2133  
Db 2018 ACTGAGATTTTCTGTATATATGTTGTTTGTAAAGATGTTTACACATACAGATGCT 2077  
Qy 2134 ATACTGTGAAAGATGTTTCAATCTTGAAAGAACATACATCATGATATGCAAGAG 2193  
Db 2078 ATACTGTGAAAGATGTTTCAATCTTGAAAGAACATACATCATGATATGCAAGAG 2137  
Qy 2194 GAGAGAA 2200  
Db 2138 GAGAGAA 2144  
  
RESULT 5  
US-09-854-133-441  
; Sequence 441, Application US/09854133  
; Publication No. US20020183499A1  
; GENERAL INFORMATION:  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Mohamath, Raodch  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; FILE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.475C10  
; CURRENT APPLICATION NUMBER: US/09/854,133  
; CURRENT FILING DATE: 2001-05-11  
; NUMBER OF SEQ ID NOS: 735  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 441  
; LENGTH: 5981  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-854-133-441  
  
Query Match 83.4%; Score 1867; DB 10; Length 5981;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 334 GAGAAAGTGCAGCTGAAGAGGAAAGTCATTTACTGAGGGAGTCTCCATATCATTTGGC 393  
Db 278 GAGAAAGTGCAGCTGAAGAGGAAAGTCATTTACTGAGGGAGTCTCCATATCATTTGGC 337  
  
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Db 338 ACCATCATTTGGAGCAGGAATCTTCATCTCTCTAAGGGGCTCTCCAGAACACGGGCAGC 397  
  
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Db 398 GTGGGCATGTCCTGACCATCTGACGCGTGTGGGGTCTCTCACTATTTGAGCTTTG 457  
  
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Db 458 TCTTATGCTGAATGGGAACAACATAAAGAAATCTGGAGGTCATACATATATTTTG 517  
  
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Db 518 GAAGTCTTTGGTCCATTACAGCTTTTGTACAGTCTGGTGGAACTCTCATATATACGC 577  
  
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Qy 874 GGTCAACGCGAGAACTTTAAAGACCCCTTTTCAGGAAGAGATTCAGATTTACGCGTTG 933  
Db 818 GGTCAACGCGAGAACTTTAAAGACCCCTTTTCAGGAAGAGATTCAGATTTACGCGTTG 877  
Qy 934 CCATCTGGCTTTTATATGGAATGTATGCAATATGCTGCTGGTCTTCTCAACTTTGTT 993  
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Db 938 ACTGAAGAAGTAGAAAACCCCTGAAAAACCAATCCCTTGAATATGATATATCCATGGCC 997  
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Db 1118 TCATTAGCAGTTCCGATCTTTGTCCTCTCTGCTTTGCTCCATGAACGGTGGTGTG 1177  
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Db 1238 TCCATGATTGATGTCGCAAGCACACTCTCTACAGCTGTTATGTTTGCACCCCTTG 1297  
Qy 1354 ACAATGATAATGCTCTCTCTGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTTCGC 1413  
Db 1298 ACAATGATAATGCTCTCTCTGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTTCGC 1357  
Qy 1414 AGTGGCTTTTATTTGGCTGGCAGTGTCTGGGCTGATTTATCTTCGATACAAATGCCA 1473  
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Db 1418 CATATGATCGTCTCTTTCAAGTGCCACTGTTTCATCCAGCTTTGTTTCTTCACATGC 1477  
Qy 1534 CTCTTCATGTTGCCCTTTCCCTCTATTTCGACCCATTTAGTACAGGGAATGGCTTCGTC 1593  
Db 1478 CTCTTCATGTTGCCCTTTCCCTCTATTTCGACCCATTTAGTACAGGGAATGGCTTCGTC 1537  
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QY 1834 ATAAACAAAGAGGAGTCAGTTATTTTATTCATATATTTTAGCATATTCGAACCTAATTTCT 1893
Db 1778 ATAAACAAAGAGGAGTCAGTTATTTTATTCATATATTTTAGCATATTCGAACCTAATTTCT 1837
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Db 1898 TGCACAAATTTTGAGTCTCTGATACCTACCTATTTGGGTTAGGAGAAAGACTAGACAA 1957
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QY 2074 ACTGAGATTTTCTGATATATGAGTTTGTAAAGATGTTTACACACTACAGATGCT 2133
Db 2018 ACTGAGATTTTCTGATATATGAGTTTGTAAAGATGTTTACACACTACAGATGCT 2077
QY 2134 ATACTGTGAAAGTGTTCATCTGAAATTTGAAAGAAAGCATATGATGAGCAAGAG 2193
Db 2078 ATACTGTGAAAGTGTTCATCTGAAATTTGAAAGAAAGCATATGATGAGCAAGAG 2137
QY 2194 GAGAGAA 2200
Db 2138 GAGAGAA 2144

RESULT 6
US-10-144-649A-441
; Sequence 441, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 441
; LENGTH: 5981
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-649A-441

Query Match 83.4%; Score 1867; DB 14; Length 5981;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 GAGAAAGTCAGCTGAGAGGAAGTCACTTACTGAGGGAGTCTCCATTCATTTGGC 393
Db 278 GAGAAAGTCAGCTGAGAGGAAGTCACTTACTGAGGGAGTCTCCATTCATTTGGC 337
QY 394 ACCATCATTTGGAGCAGGAATCTTCATCTCTCTAAGGGCGTCTCCAGAACACGGGAGC 453
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Db 398 GTGGCGATCTCTGACCATCTGACCGTGTGTGGGGTCTGTCACTATTTGGAGCTTTG 457
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QY 574 GAAGTCTTTTGGTCCATTACAGCTTTTGTACAGTCTGGTGAACCTCTCATATAAGC 633
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QY 634 CCTGAGCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTTCTGGAACCAATTTT 693
Db 578 CCTGAGCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTTCTGGAACCAATTTT 637
QY 694 ATTCAATGTGAAATCCCTGAACTTTGCGATCAAGCTCATTAAGCTGTGGGATACCTGTA 753
Db 638 ATTCAATGTGAAATCCCTGAACTTTGCGATCAAGCTCATTAAGCTGTGGGATACCTGTA 697
QY 754 GTGATGTCTTAAATPAGCATGAGTGTGAGTGTGAGCGCCGCGATCCAGATTTTCTTAACC 813
Db 698 GTGATGTCTTAAATPAGCATGAGTGTGAGTGTGAGCGCCGCGATCCAGATTTTCTTAACC 757
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QY 1414 AGTGGCTTTTATGAGCTGGAGTGTGCTGATTTATCTTCGATAAAATGCCA 1473
Db 1358 AGTGGCTTTTATGAGCTGGAGTGTGCTGATTTATCTTCGATAAAATGCCA 1417
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1658	Db		CCAGAGAGAGATAAGTTATGNACTPAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGA	1717
1774	QY		GACACAAAATAGGGATTTTACTTCAATTTCTGAAAGCTAGAGAAATTACAACCTTTGGTG	1833
1718	Db		GACACAAAATAGGGATTTTACTTCAATTTCTGAAAGCTAGAGAAATTACAACCTTTGGTG	1777
1834	QY		ATAACAAAAGGAGTCAGTTATTTTTATTCATATATTTTAGACATATTCGAACTAATTTCT	1893
1778	Db		ATAACAAAAGGAGTCAGTTATTTTTATTCATATATTTTAGCATATTTCGAACTAATTTCT	1837
1894	QY		AAGAAATTTAGTTATAAATCTATGTAGTTATATGAAAGTGAATATGCAAGTTATTTCTATGAG	1953
1838	Db		AAGAAATTTAGTTATAAATCTATGTAGTTATATGAAAGTGAATATGCAAGTTATTTCTATGAG	1897
1954	QY		TGCGACAAATCTTGAGTCTCTGATACCTACTATTTGGGGTTAGGAGAAAGACTAGACAA	2013
1898	Db		TGCGACAAATCTTTGAGTCTCTGATACCTACTATTTGGGGTTAGGAGAAAGACTAGACAA	1957
2014	QY		TTACTATGTGGTCATTTCTTACAACATATGTTAGCAGCGCAAGAAACCTTCAAATTTGAAG	2073
1958	Db		TTACTATGTGGTCATTTCTTACAACATATGTTAGCAGCGCAAGAAACCTTCAAATTTGAAG	2017
2074	QY		ACTGAGATTTTTCTGTATATATGCGTTTTGTAAAGTGGTTTTACACACTACAGATGTCT	2133
2018	Db		ACTGAGATTTTTCTGTATATATGCGTTTTGTAAAGTGGTTTTACACACTACAGATGTCT	2077
2134	QY		ATACTGTGAAAAGTGGTTTTCAAATTTCTGAAAAAGCATACATCATGATTTATGCAAGAG	2193
2078	Db		ATACTGTGAAAAGTGGTTTTCAAATTTCTGAAAAAGCATACATCATGATTTATGCAAGAG	2137
2194	QY		GAGAGAA	2200
2138	Db		GAGAGAA	2144

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RESULT 7
US-10-144-649A-740
; Sequence 740, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210421.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 740
; LENGTH: 6080
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-649A-740

Query Match      83.4%; Score 1867; DB 14; Length 6080;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      334  GAGAAAGTGCAGCTGAAGAGGAAAGTCATTTTACTGAGGGGAGTCTCCATTATCATTTGGC 393
Db      372  GAGAAAGTGCAGCTGAAGAGGAAAGTCATTTTACTGAGGGGAGTCTCCATTATCATTTGGC 431
QY      394  ACCATCATTTGGACAGGAAATCTTCATCTCTCCPAAGGGGGTGTCTCCAGAACACGGGCAGC 453

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Db	432	ACCATCATTTGGAGCAGGAATCTTTCATCTCTCTTAAGGCGGTGCTCCAGAAACACGGCGACG	491
QY	454	GTGGGCATGTCTCTGACCAATCTGAACGGTGTGTGGGTCTGTGTCACTATTTTGGAGCTTTTG	513
Db	492	GTGGGCATGTCTCTGACCAATCTGACCGTGTGTGGGTCTGTGTCACTATTTTGGAGCTTTTG	551
QY	514	TCATTATGCTGAATTTGGGAAACAACATATAAAGAAATCTGTGAGTCAATTAACACATATATTTTG	573
Db	552	TCATTATGCTGAATTTGGGAAACAACATATAAAGAAATCTGTGAGTCAATTAACACATATATTTTG	611
QY	574	GAAGTCTTTTGGTCCATTAACAGCTTTTGTACAGTCTGGGTGGAACTCCTCATATAATACGC	633
Db	612	GAAGTCTTTTGGTCCATTAACAGCTTTTGTACAGTCTGGGTGGAACTCCTCATATAATACGC	671
QY	634	CCTCGAGTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTCCTGGAACCAATTTTTT	693
Db	672	CCTCGAGTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTCCTGGAACCAATTTTTT	731
QY	694	ATTCAATGTGAAATCCCTGAACTTGCATCAAGCTCAATTACAGCTGTGGGCAATAACGTGA	753
Db	732	ATTCAATGTGAAATCCCTGAACTTGCATCAAGCTCAATTACAGCTGTGGGCAATAACGTGA	791
QY	754	GTGATGTGCTTAATAGCATGAGTGTGAGTGTGAGAGCCCGGATCCAGATTTTCTTTAAACC	813
Db	792	GTGATGTGCTTAATAGCATGAGTGTGAGTGTGAGAGCCCGGATCCAGATTTTCTTTAAACC	851
QY	814	TTTTGCAAGCTCACAGCAATCTCATTAATATATAGTCCCTGGAGTATGACGTAAATTTAAA	873
Db	852	TTTTGCAAGCTCACAGCAATCTCATTAATATATAGTCCCTGGAGTATGACGTAAATTTAAA	911
QY	874	GGTCAAAACGAGCAACTTTAAAGAGCGCTTTTCAGGAAGAGATTCAAGTATTTACCGCGTTG	933
Db	912	GGTCAAAACGAGCAACTTTAAAGAGCGCTTTTCAGGAAGAGATTCAAGTATTTACCGCGTTG	971
QY	934	CCACTGCTTTTTTATATGAATGTATGCAATGTCTGGTGGTTTTTACCTCAAATTTGTT	993
Db	972	CCACTGCTTTTTTATATGAATGTATGCAATGTCTGGTGGTTTTTACCTCAAATTTGTT	1031
QY	994	ACTGAAGAAGTAGAAAAACCTTGAAAAAACCAATTCCTCTGCAATATGATATCAATCGCC	1053
Db	1032	ACTGAAGAAGTAGAAAAACCTTGAAAAAACCAATTCCTCTGCAATATGATATCAATCGCC	1091
QY	1054	ATTGTCAACCATTTGGCTATGTGCTGCACAAATGTGGCCTACTTTACGACCAATTAATGCTGAG	1113
Db	1092	ATTGTCAACCATTTGGCTATGTGCTGCACAAATGTGGCCTACTTTACGACCAATTAATGCTGAG	1151
QY	1114	GAGCTGTGCTTTCAAATGCAAGTGGCAGTGAACCTTTTCTGAGCGGCTACTGGGAAATTTTC	1173
Db	1152	GAGCTGTGCTTTCAAATGCAAGTGGCAGTGAACCTTTTCTGAGCGGCTACTGGGAAATTTTC	1211
QY	1174	TCATTAGCACTCCGATCTTTGTCCTCTCTGCTTTGGCTCCATGACGAGTGGTGTG	1233
Db	1212	TCATTAGCACTCCGATCTTTGTCCTCTCTGCTTTGGCTCCATGACGAGTGGTGTG	1271
QY	1234	TTTGTCTGTCTCCAGGTTAATCTATGTTGGCTCTCGAGAGGCTCACCTTCAGAGAAATCCCTC	1293
Db	1272	TTTGTCTGTCTCCAGGTTAATCTATGTTGGCTCTCGAGAGGCTCACCTTCAGAGAAATCCCTC	1331
QY	1294	TCCATGATTCATGTCCGACAGACACATCCTCTTACAGCTGTATTTGTTTGGACCCCTTTG	1353
Db	1332	TCCATGATTCATGTCCGACAGACACATCCTCTTACAGCTGTATTTGTTTGGACCCCTTTG	1391
QY	1354	ACAAATGATTAATGCTCTTCTCTGAGACCTTCGACAGTCTTTTGAATTTCTCAGTTTTGGC	1413
Db	1392	ACAAATGATTAATGCTCTTCTCTGAGACCTTCGACAGTCTTTTGAATTTCTCAGTTTTGGC	1451
QY	1414	AGGTGGCTTTTTATTTGGGCTGGCAGTTGTGTGGCTCATTTATCTTCGATACAAATGCCCA	1473
Db	1452	AGGTGGCTTTTTATTTGGGCTGGCAGTTGTGTGGCTCATTTATCTTCGATACAAATGCCCA	1511
QY	1474	GATATGATCGTCCCTTTCAAGGTGCCACTGTGTCATCCGAGTGTGTTTCTTCAATGTC	1533
Db	1512	GATATGATCGTCCCTTTCAAGGTGCCACTGTGTCATCCGAGTGTGTTTCTTCAATGTC	1571



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QY 1294 TCCATGATTCAGTCCGGAAGCACACTCTCTACAGAGTGTATTTGACACCTTTG 1353
Db 1066 TCCATGATTCAGTCCGGAAGCACACTCTCTACAGAGTGTATTTGACACCTTTG 1125
QY 1354 ACAATGATTAAGTCTCTCTGGAGACTCGACAGTCTTTGAATTTCTCAGTTTGGC 1413
Db 1126 ACAATGATTAAGTCTCTCTGGAGACTCGACAGTCTTTGAATTTCTCAGTTTGGC 1185
QY 1414 AGGTGGCTTTTATTTGGGCTGGCAGTGTCTGGGCTGATTTATCTTCGATACAAATGCCA 1473
Db 1186 AGGTGGCTTTTATTTGGGCTGGCAGTGTCTGGGCTGATTTATCTTCGATACAAATGCCA 1245
QY 1474 GATATGATTCGTCCTTCAAGTGCGACATCTTCATCCAGCTTTTCTTCCTTCACATGC 1533
Db 1246 GATATGATTCGTCCTTCAAGTGCGACATCTTCATCCAGCTTTTCTTCCTTCACATGC 1305
QY 1534 CTCCTTCAATGGTTCCTTCTCCCTCTATTCGGAACCATTTAGTACAGGATTTGGCTTCGTC 1593
Db 1306 CTCCTTCAATGGTTCCTTCTCCCTCTATTCGGAACCATTTAGTACAGGATTTGGCTTCGTC 1365
QY 1594 ATCACTCTGACTGGAGTCCCTCGCTATTTATCTCTTTATATGGGACAAAGAACCCAGG 1653
Db 1366 ATCACTCTGACTGGAGTCCCTCGCTATTTATCTCTTTATATGGGACAAAGAACCCAGG 1425
QY 1654 TGGTTTGAATTAATCTCAGAGAAATACCAAGACATTAACAAATTAATCTGGAAGTTGTA 1713
Db 1426 TGGTTTGAATTAATCTCAGAGAAATACCAAGACATTAACAAATTAATCTGGAAGTTGTA 1485
QY 1714 CCAGAAAGAGATAAGTTATGAATTAATGAATCTGAGTCTGGCAATCTGCCAAGGGGA 1773
Db 1486 CCAGAAAGAGATAAGTTATGAATTAATGAATCTGAGTCTGGCAATCTGCCAAGGGGA 1545
QY 1774 GACACAAATAGGGAATTTTACTTCATTTCTGAAAGTCTAGAGAAATACAACTTTGGTG 1833
Db 1546 GACACAAATAGGGAATTTTACTTCATTTCTGAAAGTCTAGAGAAATACAACTTTGGTG 1605
QY 1834 ATAAACAAAGAGTCAAGTATTTTATTCATATATTTTATGATATTCGAACTAATTTCT 1893
Db 1606 ATAAACAAAGAGTCAAGTATTTTATTCATATATTTTATGATATTCGAACTAATTTCT 1665
QY 1894 AAGAAATTTAGTTAATCTATGATAGTATAGAAAGTGAATATCGAGTATTTCTATGAG 1953
Db 1666 AAGAAATTTAGTTAATCTATGATAGTATAGAAAGTGAATATCGAGTATTTCTATGAG 1725
QY 1954 TCGCAATTTCTGAGTCTCTGATACCTACCTATTGGGGTTAGGAGAAAGACTAGACAA 2013
Db 1726 TCGCAATTTCTGAGTCTCTGATACCTACCTATTGGGGTTAGGAGAAAGACTAGACAA 1785
QY 2014 TTACTATGTGTCTCTCTACACATATGTTAGCAAGCAAGAACCTTCAAAATGGAAG 2073
Db 1786 TTACTATGTGTCTCTCTACACATATGTTAGCAAGCAAGAACCTTCAAAATGGAAG 1845
QY 2074 ACTGAGATTTTCTGATATATGGGTTTGTAAAGATGTTTACACTACAGATGCT 2133
Db 1846 ACTGAGATTTTCTGATATATGGGTTTGTAAAGATGTTTACACTACAGATGCT 1905
QY 2134 ATACTGTGAAAGTGTCTTCAATTTGAAAAAAGCATACATCATGATATGGAAGAG 2193
Db 1906 ATACTGTGAAAGTGTCTTCAATTTGAAAAAAGCATACATCATGATATGGAAGAG 1965
QY 2194 GAGAGAA 2200
Db 1966 GAGAGAA 1972
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RESULT 9
US-10-163-866-29
; Sequence 29, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SUC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
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; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-163-866-29

Query Match          76.9%; Score 1722; DB 14; Length 2482;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1772; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 334 GAGAAAGTGCAGCTGAAGAGAGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTGGC 393
Db 337 GAGAAAGTGCAGCTGAAGAGAGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTGGC 396
QY 394 ACCATCATTTGGAGCAGAAATCTTCATCTCTCTTAAGGGCGTCTCCAGAACACAGGGCAGC 453
Db 397 ACCATCATTTGGAGCAGAAATCTTCATCTCTCTTAAGGGCGTCTCCAGAACACAGGGCAGC 456
QY 454 GTGGGCAATGCTCTGACCATCTGGAACGCTGTGTGGGGTCTCTGTCACTATTATTTGGAGCTTTG 513
Db 457 GTGGGCAATGCTCTGACCATCTGGAACGCTGTGTGGGGTCTCTGTCACTATTATTTGGAGCTTTG 516
QY 514 TCTTATGCTGAATTTGGAAACAACTATATAAGAAATCTGAGGTCAATTACACATATATTTTG 573
Db 517 TCTTATGCTGAATTTGGAAACAACTATATAAGAAATCTGAGGTCAATTACACATATATTTTG 576
QY 574 GAAGTCTTTGGTCCATTACAGAGCTTTTGTAGAGTCTGGGTGGAACTCTCATTAATACGC 633
Db 577 GAAGTCTTTGGTCCATTACAGAGCTTTTGTAGAGTCTGGGTGGAACTCTCATTAATACGC 636
QY 634 CTTGACGCTACTGCTGTGTATATCCCTGSCATTTTGGAGCTACATTTCTGGAGCACTTTT 693
Db 637 CTTGACGCTACTGCTGTGTATATCCCTGGCATTTTGGAGCTACATTTCTGGAGCACTTTT 696
QY 694 ATTCAATGTGAATFCCCTGAACTTTGCGATCAAGCTCATTACAGCTGTGGGCATTAACCTGTA 753
Db 697 ATTCAATGTGAATFCCCTGAACTTTGCGATCAAGCTCATTACAGCTGTGGGCATTAACCTGTA 756
QY 754 GTGATGTCTTAATAGCATGAGTGTGAGTGTGAGGCGCCGGATCCAGATTTTCTTAACC 813
Db 757 GTGATGTCTTAATAGCATGAGTGTGAGTGTGAGGCGCCGGATCCAGATTTTCTTAACC 816
QY 814 TTTTGCAGCTCAAGCAATTTCTGATATTAATAGTCCCTGGAGTTATGCGAGTCAATTAATAA 873
Db 817 TTTTGCAGCTCAAGCAATTTCTGATATTAATAGTCCCTGGAGTTATGCGAGTCAATTAATAA 876
QY 874 GGTCAAAACGAGAACTTTTAAAGAGCGCTTTTTCAGGAAAGAGATTCAGATTTATACCGGTTG 933
Db 877 GGTCAAAACGAGAACTTTTAAAGAGCGCTTTTTCAGGAAAGAGATTCAGATTTATACCGGTTG 936
QY 934 CCATGCTTTTATTAATGGAATGTATGATATGTGGCTGGTGTGTACCTCAACTTTGTT 993
Db 937 CCATGCTTTTATTAATGGAATGTATGATATGTGGCTGGTGTGTACCTCAACTTTGTT 996
QY 994 ACTGAGCAAGTGAAGAACCCCTGAAAAACCATTTCCCTTGCATATATGCTATATCCATGCCC 1053
Db 997 ACTGAGCAAGTGAAGAACCCCTGAAAAACCATTTCCCTTGCATATATGCTATATCCATGCCC 1056
QY 1054 ATTGTCAACCATTTGGCTATGTGCTGACAAATGTGGCCTACTTTTACGACCAATTAATGCTGAG 1113
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QY 934 CCACCTGGCTTTTATATGGAATGATGATGCTGGCTGGTTTACCTCAACTTTGTT 993
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QY 947 CCACCTGGCTTTTATATGGAATGATGATGCTGGCTGGTTTACCTCAACTTTGTT 1006
Db |||
QY 994 ACTGAAGAAGTAGAAAACCTGAAAACCAATCCCTTGCATATGATATATCCATGCCC 1053
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QY 1007 ACTGAAGAAGTAGAAAACCTGAAAACCAATCCCTTGCATATGATATATCCATGCCC 1066
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QY 1054 ATGTCAACATGGCTATGCTGACAAATGTGGCTACTTTACGACCAATTAATGCTGAG 1113
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QY 1067 ATGTCAACATGGCTATGCTGACAAATGTGGCTACTTTACGACCAATTAATGCTGAG 1126
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QY 1114 GAGCTGCTCTTCAAAATGACGAGTACCTTTCTGACGGCTACTGGAATTTTC 1173
Db |||
QY 1127 GAGCTGCTCTTCAAAATGACGAGTACCTTTCTGACGGCTACTGGAATTTTC 1186
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QY 1174 TCATTAGCAGTTCCGATCTTTCTGCGCTCTCTGCTTGGCTCCATGAACGGTGGTG 1233
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QY 1187 TCATTAGCAGTTCCGATCTTTCTGCGCTCTCTGCTTGGCTCCATGAACGGTGGTG 1246
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QY 1234 TTGCTGCTCCAGTTATCTTATGTTGGCTCGAGGGTCACTTCCAGAAATCTC 1293
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QY 1247 TTGCTGCTCCAGTTATCTTATGTTGGCTCGAGGGTCACTTCCAGAAATCTC 1306
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QY 1294 TCATGATTCATGTCGGAAGCACACTCTCTACAGCTGTTATTTGTTGACCCCTTG 1353
Db |||
QY 1307 TCATGATTCATGTCGGAAGCACACTCTCTACAGCTGTTATTTGTTGACCCCTTG 1366
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QY 1354 ACAATGATAATGCTCTCTCGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTGGC 1413
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QY 1367 ACAATGATAATGCTCTCTCGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTGGC 1426
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QY 1414 AGGTGGCTTTTATTTGGGCTGCGAGTGTGCTGGCTGATTAATCTTCGATCAAAATGCCA 1473
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QY 1427 AGGTGGCTTTTATTTGGGCTGCGAGTGTGCTGGCTGATTAATCTTCGATCAAAATGCCA 1486
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QY 1474 GATATGATCGTCCCTTTCAAGGTGCCACTGTTTCATCCAGCTTGTGTTTCTTCACATGC 1533
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QY 1487 GATATGATCGTCCCTTTCAAGGTGCCACTGTTTCATCCAGCTTGTGTTTCTTCACATGC 1546
Db |||
QY 1534 CTCTTCATGGTGGCTTTCCCTCTATTTCGGACCCATTTAGTACAGGATGGCTTCGTC 1593
Db |||
QY 1547 CTCTTCATGGTGGCTTTCCCTCTATTTCGGACCCATTTAGTACAGGATGGCTTCGTC 1606
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QY 1594 ATCACTCTGACGTGAGTCCCTCGTATTAATCTCTTTATATATGAGCAAGAACCCAGG 1653
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QY 1607 ATCACTCTGACGTGAGTCCCTCGTATTAATCTCTTTATATATGAGCAAGAACCCAGG 1666
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QY 1654 TGGTTTGAATAATGTCAGAGAAAATAACCAACATTAACAAATAATCTGGAAGTTGTA 1713
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QY 1667 TGGTTTGAATAATGTCAGAGAAAATAACCAACATTAACAAATAATCTGGAAGTTGTA 1726
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QY 1714 CCAGAGAAGATAGTTATGAACTTAATGGAATTTGAGATCTTGGCAATCTGCCAAGGGGA 1773
Db |||
QY 1727 CCAGAGAAGATAGTTATGAACTTAATGGAATTTGAGATCTTGGCAATCTGCCAAGGGGA 1786
Db |||
QY 1774 GACACAAAATAGGGATTTTACTTCAATTTCTGAAGTCTAGAGAAATTAACACTTTGGTG 1833
Db |||
QY 1787 GACACAAAATAGGGATTTTACTTCAATTTCTGAAGTCTAGAGAAATTAACACTTTGGTG 1846
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QY 1834 ATAAACAAAAGGAGTCAGTTATTTTATCATATATTTTAGCATATTCGAATTAATTTCT 1893
Db |||
QY 1847 ATAAACAAAAGGAGTCAGTTATTTTATCATATATTTTAGCATATTCGAATTAATTTCT 1906
Db |||
QY 1894 AAGAAATTTAGTTATACTATGATGATTAAGAAAGTGAATATGCACTTTCTATGAG 1953
Db |||
QY 1907 AAGAAATTTAGTTATATCTATGATGATTAAGAAAGTGAATATGCACTTTCTATGAG 1966
Db |||
QY 1954 TCGCACAAATCTTGAGTCTCTGATACCTACC 1984
Db |||
QY 1967 TCGCACAAATCTTGAGTCTCTGATACCTACC 1997
Db |||
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## RESULT 12

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US-10-163-866-30
; Sequence 30, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1861
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-163-866-30
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Query Match 64.98; Score 1454; DB 14; Length 1861;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1504; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 334 GAGAAATGCGAGTGAAGAGGAAGTCACTTTACTAGGGAGTCTCCATTATCATTTGGC 393
Db |||
QY 341 GAGAAATGCGAGTGAAGAGGAAGTCACTTTACTAGGGAGTCTCCATTATCATTTGGC 400
Db |||
QY 394 ACATATGTTGAGCAGGAATCTTCATCTCTTAAGGGCTGCTCCAGAACACGGGAGC 453
Db |||
QY 401 ACCATCATTTGAGCAGGAATCTTCATCTCTTAAGGGCTGCTCCAGAACACGGGAGC 460
Db |||
QY 454 GTGGGCATGTCCTGACCATCTGGACGATGTTGGGCTGCTGTCATTTTGGAGCTTTG 513
Db |||
QY 461 GTGGGCATGTCCTGACCATCTGGACGATGTTGGGCTGCTGTCATTTTGGAGCTTTG 520
Db |||
QY 514 TCTTATGCTGAATTTGGGAACAACCTATAAAGAAATCTGAGGTCAATTACATATATTTTG 573
Db |||
QY 521 TCTTATGCTGAATTTGGGAACAACCTATAAAGAAATCTGAGGTCAATTACATATATTTTG 580
Db |||
QY 574 GAAGTCTTTTGGTCCATTTACCAGCTTTTGTACGAGTCTGGGTGGAACCTCCTCATTAACGC 633
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QY 581 GAAGTCTTTTGGTCCATTTACCAGCTTTTGTACGAGTCTGGGTGGAACCTCCTCATTAACGC 640
Db |||
QY 634 CTTGACGCTACTGCTGTGATATCCCTGGCATTTTGGACGCTACATTTCTGGAACCAATTTT 693
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QY 641 CTTGACGCTACTGCTGTGATATCCCTGGCATTTTGGACGCTACATTTCTGGAACCAATTTT 700
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QY 694 ATTCAATGTAATTCCTGAACTTGGATCAAGTCAAGTCAATTACAGCTGTGGGCATAACTGTA 753
Db |||
QY 701 ATTCAATGTAATTCCTGAACTTGGATCAAGTCAAGTCAATTACAGCTGTGGGCATAACTGTA 760
Db |||
QY 754 GTGATGTCCTTAATAGCATGAGTGTGAGTGTGAGCGCCCGGATCCAGATTTTCTTAACC 813
Db |||
QY 761 GTGATGTCCTTAATAGCATGAGTGTGAGTGTGAGCGCCCGGATCCAGATTTTCTTAACC 820
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QY 814 TTTTGAAGCTCACAGCAATTTCTGATAATTTATAGTCCCTGGAGTTATGAGCTAATTTAA 873
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QY 821 TTTTGAAGCTCACAGCAATTTCTGATAATTTATAGTCCCTGGAGTTATGAGCTAATTTAA 880
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QY 874 GGTCAAAACGAGAACTTTAAAGACGCTTTTTCAGGAAGAGATTCAGATTAATACCGGTTG 933
Db |||
QY 881 GGTCAAAACGAGAACTTTAAAGACGCTTTTTCAGGAAGAGATTCAGATTAATACCGGTTG 940
Db |||
QY 934 CCACTGGCTTTTATATGGAATGATGATATGCTGGCTGGTTTACCTCAACTTTGTT 993
Db |||
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Db 941 CCACGGCTTTTATTATGAATGATGATATGCTGCTGGTGGTTTCTCAACTTTGT 1000
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Db 1001 ACTGAAGAGTAGAAAACCTGAAAAACCATTCCTTGCATATGATATATCCATGACC 1060
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Db 1061 ATTGTACCAATGGCTATGTGCTGACAAATGTGGCTACTTTACACCAATTAATGCTGAG 1120
Qy 1114 GAGCTGCTTTTCAAATGACAGTGCAGTACCTTTTCTGAGCGCTACTGGGAATTTTC 1173
Db 1121 GAGCTGCTTTTCAAATGACAGTGCAGTACCTTTTCTGAGCGCTACTGGGAATTTTC 1180
Qy 1174 TCATTAGCAGTTCCGATCTTTGCTCCCTCCCTGCTTGGCTCCATGAACGGTGGTG 1233
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Qy 1474 GATATGATCGTCTTTCAAGTGCCACTGTCTATCCGAGCTTTGTTTCTTTCATGTC 1533
Db 1481 GATATGATCGTCTTTCAAGTGCCACTGTCTATCCGAGCTTTGTTTCTTTCATGTC 1540
Qy 1534 CTCCTTCAAGTGGCTTCCCTCTATTCGGACCATTTAGTACAGGATTTGGCTTCGTC 1593
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; Sequence 33, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
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; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-163-866-33

Query Match 63.4%; Score 1420; DB 14; Length 1542;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence S2, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/10/163,866
; FILE REFERENCE: EX02-080C
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 1528
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-163-866-52

Query Match 58.0%; Score 1299; DB 14; Length 1528;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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108	7	1.0	130	1	US-08-716-588-4	Sequence 4, Appli	C 181	7	1.0	371	3	US/08/622	INFORMATION FOR
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110	7	1.0	130	2	US-08-966-444-4	Sequence 4, Appli	C 183	7	1.0	374	4	US-09-252-991A-22425	Sequence 22425, A
111	7	1.0	130	2	US-08-966-444-5	Sequence 5, Appli	C 184	7	1.0	376	4	US-09-252-991A-28256	Sequence 28256, A
112	7	1.0	130	3	US-08-398-633-13	Sequence 13, Appl	C 185	7	1.0	380	4	US-09-198-452A-234	Sequence 234, App
113	7	1.0	130	3	US-08-398-633-14	Sequence 14, Appl	C 186	7	1.0	391	4	US-09-107-532A-4419	Sequence 4419, Ap
114	7	1.0	130	3	US-08-480-070C-13	Sequence 13, Appl	C 187	7	1.0	392	4	US-09-071-035-260	Sequence 260, App
115	7	1.0	130	3	US-08-480-070C-14	Sequence 14, Appl	C 188	7	1.0	406	4	US-09-599-360B-98	Sequence 98, Appl
116	7	1.0	130	3	US-08-829-525-13	Sequence 13, Appl	C 189	7	1.0	409	4	US-09-198-452A-554	Sequence 554, App
117	7	1.0	130	3	US-08-829-525-14	Sequence 14, Appl	C 190	7	1.0	414	4	US-09-134-001C-3357	Sequence 3357, Ap
118	7	1.0	130	3	US-08-609-583A-13	Sequence 13, Appl	C 191	7	1.0	418	3	US-09-030-267-5	Sequence 5, Appli
119	7	1.0	130	3	US-08-609-583A-14	Sequence 14, Appl	C 192	7	1.0	420	2	US-08-466-103A-2	Sequence 2, Appli
120	7	1.0	130	3	US-08-937-399-13	Sequence 13, Appl	C 193	7	1.0	435	4	US-09-252-991A-17254	Sequence 17254, A
121	7	1.0	130	3	US-08-937-399-14	Sequence 14, Appl	C 194	7	1.0	437	4	US-09-252-991A-17213	Sequence 17213, A
122	7	1.0	130	4	US-09-310-367-13	Sequence 13, Appl	C 195	7	1.0	449	4	US-09-107-532A-5466	Sequence 5466, Ap
123	7	1.0	130	4	US-09-310-367-14	Sequence 14, Appl	C 196	7	1.0	465	4	US-09-252-991A-20576	Sequence 20576, A
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125	7	1.0	130	4	US-09-032-337-14	Sequence 14, Appl	C 198	7	1.0	466	3	US-08-868-435-12	Sequence 12, Appl
126	7	1.0	130	4	US-09-464-231-13	Sequence 13, Appl	C 199	7	1.0	466	4	US-08-744-231-2	Sequence 2, Appli
127	7	1.0	130	4	US-09-464-231-14	Sequence 14, Appl	C 200	7	1.0	466	4	US-08-744-231-12	Sequence 12, Appl
128	7	1.0	131	4	US-09-252-991A-29620	Sequence 29620, A	C 201	7	1.0	466	4	US-09-636-499-7	Sequence 7, Appli
C 129	7	1.0	139	4	US-09-328-352-8016	Sequence 8016, Ap	C 202	7	1.0	466	4	US-09-373-871A-12	Sequence 12, Appl
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C 131	7	1.0	140	3	US-08-569-147-89	Sequence 82, Appl	C 204	7	1.0	483	4	US-09-384-212-2	Sequence 2, Appli
C 132	7	1.0	140	4	US-09-252-991A-31652	Sequence 31652, A	C 205	7	1.0	487	4	US-09-252-991A-23912	Sequence 23912, A
C 133	7	1.0	140	4	US-09-107-532A-4699	Sequence 4699, Ap	C 206	7	1.0	488	3	US-08-942-012B-29	Sequence 29, Appl
C 134	7	1.0	152	4	US-09-252-991A-28263	Sequence 28263, A	C 207	7	1.0	488	3	US-08-942-012B-30	Sequence 30, Appl
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C 136	7	1.0	155	4	US-09-252-991A-20099	Sequence 20099, A	C 209	7	1.0	494	4	US-09-252-991A-28873	Sequence 28873, A
C 137	7	1.0	156	4	US-09-252-991A-30401	Sequence 30401, A	C 210	7	1.0	498	4	US-09-328-352-7320	Sequence 7320, Ap
C 138	7	1.0	157	4	US-09-252-991A-18044	Sequence 18044, A	C 211	7	1.0	501	4	US-09-134-001C-5280	Sequence 5280, Ap
C 139	7	1.0	160	4	US-09-615-132A-341	Sequence 341, App	C 212	7	1.0	502	1	US-08-484-840-3	Sequence 3, Appli
C 140	7	1.0	162	4	US-09-252-991A-23275	Sequence 23275, A	C 213	7	1.0	502	1	US-08-483-094-3	Sequence 3, Appli
C 141	7	1.0	177	4	US-09-252-991A-29815	Sequence 29815, A	C 214	7	1.0	503	1	US-08-484-840-4	Sequence 4, Appli
C 142	7	1.0	177	5	US-08-867-030B-16	Sequence 16, Appl	C 215	7	1.0	503	1	US-08-483-094-4	Sequence 4, Appli
C 143	7	1.0	177	5	PCT-US95-06119-16	Sequence 16, Appl	C 216	7	1.0	511	3	US-08-278-635B-8	Sequence 8, Appli
C 144	7	1.0	182	4	US-09-523-686-3	Sequence 3, Appli	C 217	7	1.0	511	3	US-08-464-258B-8	Sequence 8, Appli
C 145	7	1.0	191	4	US-09-252-991A-25365	Sequence 25365, A	C 218	7	1.0	511	3	US-08-471-961-8	Sequence 8, Appli
C 146	7	1.0	202	4	US-09-252-991A-28110	Sequence 28110, A	C 219	7	1.0	516	2	US-08-794-216-3	Sequence 3, Appli
C 147	7	1.0	211	1	US-08-428-415-8	Sequence 8, Appli	C 220	7	1.0	516	2	US-08-749-289-3	Sequence 3, Appli
C 148	7	1.0	211	2	US-08-379-685-8	Sequence 8, Appli	C 221	7	1.0	516	4	US-09-198-452A-598	Sequence 598, App
C 149	7	1.0	211	2	US-08-854-029-8	Sequence 8, Appli	C 222	7	1.0	521	4	US-09-071-035-64	Sequence 64, Appl
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C 152	7	1.0	236	4	US-09-252-991A-27285	Sequence 27285, A	C 225	7	1.0	526	4	US-09-252-991A-20533	Sequence 20533, A
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C 154	7	1.0	241	2	US-08-825-781-4	Sequence 4, Appli	C 227	7	1.0	541	4	US-09-252-991A-24521	Sequence 24521, A
C 155	7	1.0	245	2	US-08-825-781-1	Sequence 1, Appli	C 228	7	1.0	542	4	US-09-071-035-62	Sequence 62, Appl
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C 237 585 2 US-08-869-477-6 Sequence 6, Appl  
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C 273 882 4 US-09-252-991A-17653 Sequence 17653, A  
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C 369 6 8 US-09-128-344A-162 Sequence 162, App  
C 370 6 8 US-09-128-344A-169 Sequence 169, App  
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C 374 6 8 PCT-US91-05047-32 Sequence 32, Appl  
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C 376 6 8 PCT-US91-05047-40 Sequence 40, Appl  
C 377 6 8 PCT-US95-07543-4 Sequence 4, Appl



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380	6	0.8	20	1	US-08-289-653-3	Sequence 3, Appl	453	6	0.8	36	4	US-08-467-344A-245	Sequence 245, App
381	6	0.8	20	1	US-07-678-974D-54	Sequence 54, Appl	454	6	0.8	37	1	US-08-313-681A-6	Sequence 6, Appl
382	6	0.8	20	1	US-08-222-851-35	Sequence 35, Appl	455	6	0.8	37	2	US-08-505-486-97	Sequence 97, Appl
383	6	0.8	20	1	US-08-222-851-36	Sequence 36, Appl	456	6	0.8	37	3	US-08-801-028-97	Sequence 97, Appl
384	6	0.8	20	1	US-08-934-915-73	Sequence 73, Appl	457	6	0.8	37	3	US-09-340-154-97	Sequence 97, Appl
385	6	0.8	20	2	US-08-945-168-60	Sequence 60, Appl	458	6	0.8	37	3	US-09-322-911-6	Sequence 6, Appl
386	6	0.8	20	3	US-08-861-338-8	Sequence 8, Appl	c 459	6	0.8	37	4	US-09-149-476-741	Sequence 741, App
387	6	0.8	20	4	US-08-651-650-21	Sequence 21, Appl	460	6	0.8	37	4	US-09-482-611B-97	Sequence 97, Appl
388	6	0.8	20	4	US-08-651-650-22	Sequence 22, Appl	461	6	0.8	37	4	US-09-060-299-10	Sequence 10, Appl
389	6	0.8	21	2	US-08-400-115-7	Sequence 7, Appl	462	6	0.8	37	4	US-09-402-923A-10	Sequence 10, Appl
390	6	0.8	21	3	US-08-851-843A-175	Sequence 175, App	463	6	0.8	37	5	PCT-US95-0933A-97	Sequence 97, Appl
391	6	0.8	21	3	US-08-974-549A-294	Sequence 294, App	464	6	0.8	37	5	PCT-US95-09339-97	Sequence 97, Appl
392	6	0.8	21	3	US-08-854-050-175	Sequence 175, App	465	6	0.8	39	4	US-09-060-293-16	Sequence 16, Appl
393	6	0.8	21	4	US-09-430-323-175	Sequence 175, App	466	6	0.8	39	4	US-09-402-923A-16	Sequence 16, Appl
394	6	0.8	22	2	US-08-360-606B-12	Sequence 12, Appl	467	6	0.8	41	2	US-08-751-767A-74	Sequence 74, Appl
395	6	0.8	22	3	US-08-940-095-155	Sequence 155, App	468	6	0.8	41	3	US-08-993-165-9	Sequence 9, Appl
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397	6	0.8	22	3	US-09-276-202-5	Sequence 5, Appl	470	6	0.8	41	4	US-09-540-448-9	Sequence 9, Appl
398	6	0.8	22	3	US-09-276-202-9	Sequence 9, Appl	471	6	0.8	41	4	US-09-243-640-7	Sequence 7, Appl
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402	6	0.8	22	4	US-09-453-838-155	Sequence 155, App	475	6	0.8	42	3	US-08-441-935-19	Sequence 19, Appl
403	6	0.8	22	4	US-08-940-136-155	Sequence 155, App	476	6	0.8	42	3	US-08-441-935-21	Sequence 21, Appl
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405	6	0.8	23	3	US-08-468-011A-28	Sequence 28, Appl	c 478	6	0.8	42	3	US-08-905-223-333	Sequence 333, App
406	6	0.8	23	3	US-09-276-202-11	Sequence 11, Appl	479	6	0.8	42	3	US-08-441-943-17	Sequence 17, Appl
407	6	0.8	23	3	US-09-236-468A-28	Sequence 28, Appl	480	6	0.8	42	3	US-08-441-943-19	Sequence 19, Appl
408	6	0.8	24	2	US-08-752-891-7	Sequence 7, Appl	481	6	0.8	42	3	US-08-441-943-21	Sequence 21, Appl
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411	6	0.8	24	3	US-09-466-854-7	Sequence 7, Appl	c 484	6	0.8	43	3	US-09-273-685-40	Sequence 40, Appl
412	6	0.8	25	5	PCT-US92-07865-25	Sequence 25, Appl	485	6	0.8	43	4	US-07-757-022B-12	Sequence 12, Appl
413	6	0.8	26	4	US-08-432-483A-1	Sequence 1, Appl	c 486	6	0.8	43	4	US-09-489-847-225	Sequence 225, App
414	6	0.8	26	4	US-08-469-360A-557	Sequence 557, App	487	6	0.8	43	5	PCT-US95-11934-40	Sequence 40, Appl
415	6	0.8	26	4	US-08-945-289-1	Sequence 1, Appl	488	6	0.8	44	4	US-09-406-045-4	Sequence 4, Appl
416	6	0.8	26	4	US-08-488-446-557	Sequence 557, App	489	6	0.8	45	3	US-08-441-935-13	Sequence 13, Appl
417	6	0.8	26	4	US-08-467-344A-557	Sequence 557, App	490	6	0.8	45	3	US-08-441-935-15	Sequence 15, Appl
418	6	0.8	27	2	US-08-394-600B-4	Sequence 4, Appl	491	6	0.8	45	3	US-08-602-999A-48	Sequence 48, Appl
419	6	0.8	27	2	US-09-276-202-2	Sequence 2, Appl	492	6	0.8	45	3	US-08-441-943-13	Sequence 13, Appl
420	6	0.8	27	3	US-09-276-202-3	Sequence 3, Appl	493	6	0.8	45	3	US-08-441-943-15	Sequence 15, Appl
421	6	0.8	27	3	US-09-276-202-4	Sequence 4, Appl	494	6	0.8	45	3	US-08-278-865-48	Sequence 48, Appl
422	6	0.8	27	3	US-09-276-202-8	Sequence 8, Appl	495	6	0.8	45	4	US-09-500-124-48	Sequence 48, Appl
423	6	0.8	27	3	US-08-856-383-5	Sequence 5, Appl	496	6	0.8	45	4	US-09-288-143-110	Sequence 110, App
424	6	0.8	27	4	US-09-360-237-57	Sequence 57, Appl	497	6	0.8	46	3	US-08-928-213B-52	Sequence 52, Appl
425	6	0.8	27	4	US-09-475-088-5	Sequence 5, Appl	498	6	0.8	46	4	US-09-461-325-164	Sequence 164, App
426	6	0.8	27	4	US-08-395-456C-4	Sequence 4, Appl	499	6	0.8	47	3	US-08-975-080-13	Sequence 13, Appl
427	6	0.8	27	5	PCT-US95-02513-4	Sequence 4, Appl	500	6	0.8	47	4	US-08-679-493A-168	Sequence 168, App
428	6	0.8	27	6	5171680-14	Patent No. 5171680	501	6	0.8	47	4	US-09-187-789-43	Sequence 43, Appl
429	6	0.8	28	3	US-09-045-632-95	Sequence 95, Appl	502	6	0.8	47	4	US-09-139-600-38	Sequence 38, Appl
430	6	0.8	28	3	US-08-405-647B-39	Sequence 39, Appl	c 503	6	0.8	48	4	US-09-489-847-172	Sequence 172, App
431	6	0.8	28	3	US-08-985-499-39	Sequence 39, Appl	c 504	6	0.8	49	2	US-08-400-115-9	Sequence 9, Appl
432	6	0.8	28	5	PCT-US96-03180-39	Sequence 39, App	505	6	0.8	49	4	US-09-205-258-556	Sequence 556, App
433	6	0.8	29	4	US-09-288-143-150	Sequence 150, App	506	6	0.8	50	3	US-08-928-213B-82	Sequence 82, Appl
434	6	0.8	30	2	US-08-473-475A-3	Sequence 3, Appl	c 507	6	0.8	52	4	US-09-461-325-221	Sequence 221, App
435	6	0.8	30	3	US-08-335-844A-16	Sequence 16, Appl	c 508	6	0.8	52	4	US-09-205-258-1045	Sequence 1045, Ap
436	6	0.8	30	4	US-09-129-366-16	Sequence 16, Appl	509	6	0.8	54	4	US-09-015-030-2	Sequence 2, Appl
437	6	0.8	30	4	US-09-904-196B-7	Sequence 7, Appl	c 510	6	0.8	54	4	US-09-015-030-3	Sequence 3, Appl
438	6	0.8	33	3	US-08-341-018-10	Sequence 10, Appl	c 511	6	0.8	55	4	US-09-904-615-94	Sequence 94, Appl
439	6	0.8	33	3	US-08-470-335-209	Sequence 209, App	512	6	0.8	56	2	US-08-323-449B-4	Sequence 4, Appl
440	6	0.8	33	3	US-08-470-339-209	Sequence 209, App	513	6	0.8	56	2	US-08-485-981-4	Sequence 4, Appl
441	6	0.8	33	4	US-09-149-476-447	Sequence 447, App	514	6	0.8	56	2	US-08-867-087B-5	Sequence 5, Appl
442	6	0.8	33	4	US-08-467-602-206	Sequence 206, App	515	6	0.8	57	3	US-09-177-249-117	Sequence 117, App
443	6	0.8	33	4	US-08-467-602-403	Sequence 403, App	516	6	0.8	60	4	US-09-227-357-227	Sequence 227, App
444	6	0.8	33	4	US-08-469-260A-172	Sequence 172, App	c 517	6	0.8	61	4	US-09-227-357-256	Sequence 256, App
445	6	0.8	33	4	US-08-488-446-172	Sequence 172, App	518	6	0.8	61	4	US-09-107-532A-3795	Sequence 3795, Ap
446	6	0.8	33	4	US-08-467-344A-172	Sequence 172, App	519	6	0.8	62	1	US-08-644-664B-32	Sequence 32, Appl
447	6	0.8	33	4	US-09-205-258-323	Sequence 323, App	c 520	6	0.8	62	2	US-08-844-153-6	Sequence 6, Appl
448	6	0.8	35	2	US-08-400-115-8	Sequence 8, Appl	521	6	0.8	62	2	US-08-761-277A-32	Sequence 32, Appl
449	6	0.8	35	2	US-08-867-087B-61	Sequence 61, Appl	c 522	6	0.8	63	2	US-08-400-115-10	Sequence 10, Appl
450	6	0.8	36	4	US-08-469-260A-245	Sequence 245, App	c 523	6	0.8	63	4	US-09-690-454-52	Sequence 52, Appl

C 524	6	0.8	63	4	US-09-328-352-5729	Sequence 5729, Ap	C 597	6	0.8	74	4	US-09-252-991A-28270	Sequence 28270, A
C 525	6	0.8	64	3	US-08-789-333P-36	Sequence 26, Appl	598	6	0.8	74	4	US-09-328-352-4337	Sequence 4337, Ap
C 526	6	0.8	64	3	US-09-169-015-36	Sequence 36, Appl	C 599	6	0.8	75	3	US-08-927-219-51	Sequence 51, Appl
C 527	6	0.8	64	3	US-09-133-944-25	Sequence 25, Appl	600	6	0.8	75	3	US-08-803-346-59	Sequence 59, Appl
C 528	6	0.8	64	4	US-09-208-827-27	Sequence 27, Appl	C 601	6	0.8	75	3	US-08-803-346-60	Sequence 60, Appl
C 529	6	0.8	64	4	US-08-787-738B-26	Sequence 26, Appl	C 602	6	0.8	75	4	US-09-288-143-205	Sequence 205, Appl
C 530	6	0.8	64	4	US-09-157-748-28	Sequence 28, Appl	C 603	6	0.8	75	4	US-08-657-759-22	Sequence 22, Appl
C 531	6	0.8	64	4	US-09-800-170-79	Sequence 79, Appl	C 604	6	0.8	75	4	US-09-252-991A-22145	Sequence 22145, A
C 532	6	0.8	64	4	US-09-626-581D-39	Sequence 39, Appl	C 605	6	0.8	76	3	US-08-545-860D-57	Sequence 57, Appl
C 533	6	0.8	64	4	US-09-415-765B-39	Sequence 39, Appl	C 606	6	0.8	76	3	US-08-545-860D-92	Sequence 92, Appl
C 534	6	0.8	64	4	US-09-626-580C-39	Sequence 39, Appl	C 607	6	0.8	76	3	US-08-956-307B-18	Sequence 18, Appl
C 535	6	0.8	64	4	US-09-732-210-503	Sequence 503, Ap	C 608	6	0.8	76	3	US-08-803-346-61	Sequence 61, Appl
C 536	6	0.8	65	4	US-09-461-325-457	Sequence 457, Ap	C 609	6	0.8	76	4	US-09-180-827-2	Sequence 2, Appl
C 537	6	0.8	65	6	5320958-10	Patent No. 5320958	C 610	6	0.8	76	4	US-09-663-600A-115	Sequence 115, Appl
C 538	6	0.8	66	1	US-07-626-618A-16	Sequence 16, Appl	C 611	6	0.8	76	4	US-09-663-600A-209	Sequence 209, Appl
C 539	6	0.8	66	1	US-07-928-611-16	Sequence 16, Appl	C 612	6	0.8	76	5	PCT-US94-04496-57	Sequence 57, Appl
C 540	6	0.8	66	1	US-08-333-977-16	Sequence 16, Appl	C 613	6	0.8	77	4	US-09-328-352-7539	Sequence 7539, Ap
C 541	6	0.8	66	2	US-08-487-811A-16	Sequence 16, Appl	C 614	6	0.8	78	4	US-09-328-352-5972	Sequence 5972, Ap
C 542	6	0.8	66	3	US-09-060-69A-16	Sequence 16, Appl	C 615	6	0.8	79	3	US-09-410-028-4	Sequence 4, Appl
C 543	6	0.8	66	4	US-09-378-07A-16	Sequence 16, Appl	C 616	6	0.8	79	4	US-09-712-210-1188	Sequence 1188, Ap
C 544	6	0.8	66	4	US-09-205-258-381	Sequence 381, Appl	C 617	6	0.8	80	4	US-03-227-357-249	Sequence 249, Appl
C 545	6	0.8	66	4	US-09-252-991A-16585	Sequence 16585, A	C 618	6	0.8	80	4	US-09-183-861-61	Sequence 61, Appl
C 546	6	0.8	66	4	US-09-328-352-6899	Sequence 6899, Ap	C 619	6	0.8	80	4	US-09-022-765-61	Sequence 61, Appl
C 547	6	0.8	66	5	PCT-US93-07370-16	Sequence 16, Appl	C 620	6	0.8	80	4	US-09-551-974A-61	Sequence 61, Appl
C 548	6	0.8	67	1	US-08-307-499-16	Sequence 16, Appl	C 621	6	0.8	80	4	US-09-107-532A-6963	Sequence 6963, Ap
C 549	6	0.8	67	1	US-08-471-780C-126	Sequence 126, Appl	C 622	6	0.8	81	4	US-09-439-554-2	Sequence 2, Appl
C 550	6	0.8	67	2	US-08-467-282B-126	Sequence 126, Appl	C 623	6	0.8	82	4	US-09-500-569-24	Sequence 24, Appl
C 551	6	0.8	67	2	US-08-471-282A-126	Sequence 126, Appl	C 624	6	0.8	82	4	US-03-205-258-403	Sequence 403, Appl
C 552	6	0.8	67	2	US-08-466-710C-126	Sequence 126, Appl	C 625	6	0.8	82	4	US-09-252-991A-32127	Sequence 32127, A
C 553	6	0.8	67	3	US-08-468-739C-126	Sequence 126, Appl	C 626	6	0.8	83	3	US-08-341-018-12	Sequence 12, Appl
C 554	6	0.8	67	3	US-09-299-268-16	Sequence 16, Appl	C 627	6	0.8	83	3	US-08-470-335-198	Sequence 198, Appl
C 555	6	0.8	67	4	US-09-328-352-4211	Sequence 4211, Ap	C 628	6	0.8	83	3	US-08-470-339-198	Sequence 198, Appl
C 556	6	0.8	68	4	US-09-257-179-55	Sequence 55, Appl	C 629	6	0.8	83	4	US-08-467-602-392	Sequence 392, Appl
C 557	6	0.8	68	4	US-09-205-258-329	Sequence 329, Appl	C 630	6	0.8	84	1	US-08-452-582B-7	Sequence 7, Appl
C 558	6	0.8	68	4	US-09-107-532A-6707	Sequence 6707, Ap	C 631	6	0.8	84	4	US-09-732-210-1741	Sequence 1741, Ap
C 559	6	0.8	69	1	US-09-107-532A-6922	Sequence 6922, Ap	C 632	6	0.8	85	2	US-08-480-229C-4	Sequence 4, Appl
C 560	6	0.8	69	1	US-08-036-555B-171	Sequence 171, Appl	C 633	6	0.8	85	2	US-08-659-235C-4	Sequence 4, Appl
C 561	6	0.8	69	1	US-08-469-569-171	Sequence 171, Appl	C 634	6	0.8	85	4	US-09-134-001C-4532	Sequence 4532, Ap
C 562	6	0.8	69	1	US-08-249-322A-171	Sequence 171, Appl	C 635	6	0.8	85	4	US-09-328-352-7252	Sequence 7252, Ap
C 563	6	0.8	69	1	US-08-469-526A-171	Sequence 171, Appl	C 636	6	0.8	85	4	US-09-732-210-1119	Sequence 1119, Ap
C 564	6	0.8	69	2	US-08-469-526A-171	Sequence 171, Appl	C 637	6	0.8	85	4	US-09-107-532A-4428	Sequence 4428, Ap
C 565	6	0.8	69	2	US-08-734-591A-171	Sequence 171, Appl	C 638	6	0.8	85	4	US-09-107-532A-6944	Sequence 6944, Ap
C 566	6	0.8	69	2	US-08-583-569-1	Sequence 1, Appl	C 639	6	0.8	86	3	US-09-382-155-8	Sequence 8, Appl
C 567	6	0.8	69	2	US-08-469-660-171	Sequence 171, Appl	C 640	6	0.8	86	3	US-09-074-044A-8	Sequence 8, Appl
C 568	6	0.8	69	3	US-08-341-018-73	Sequence 73, Appl	C 641	6	0.8	87	4	US-09-134-001C-5497	Sequence 5497, Ap
C 569	6	0.8	69	3	US-08-470-335-171	Sequence 171, Appl	C 642	6	0.8	88	3	US-09-045-632-7	Sequence 7, Appl
C 570	6	0.8	69	3	US-08-735-021-171	Sequence 171, Appl	C 643	6	0.8	88	4	US-09-134-001C-2855	Sequence 2855, Ap
C 571	6	0.8	69	3	US-08-734-664A-171	Sequence 171, Appl	C 644	6	0.8	89	4	US-08-793-273C-8	Sequence 8, Appl
C 572	6	0.8	69	3	US-08-905-223-419	Sequence 419, Appl	C 645	6	0.8	89	4	US-08-793-273C-8	Sequence 8, Appl
C 573	6	0.8	69	4	US-08-467-602-171	Sequence 171, Appl	C 646	6	0.8	89	5	PCT-US95-11684-8	Sequence 8, Appl
C 574	6	0.8	69	4	US-09-328-352-4927	Sequence 4927, Ap	C 647	6	0.8	90	4	US-09-198-452A-283	Sequence 283, Appl
C 575	6	0.8	69	5	PCT-US94-05083C-167	Sequence 167, Appl	C 648	6	0.8	90	4	US-09-107-532A-6226	Sequence 6226, Ap
C 576	6	0.8	69	5	PCT-US95-06846A-171	Sequence 171, Appl	C 649	6	0.8	91	2	US-08-479-078-10	Sequence 10, Appl
C 577	6	0.8	70	4	US-09-205-258-298	Sequence 298, Appl	C 650	6	0.8	91	2	US-08-598-873-19	Sequence 19, Appl
C 578	6	0.8	70	4	US-09-107-532A-7182	Sequence 7182, Ap	C 651	6	0.8	91	3	US-08-603-430-19	Sequence 19, Appl
C 579	6	0.8	71	2	US-08-812-003-9	Sequence 9, Appl	C 652	6	0.8	92	2	US-08-273-146-45	Sequence 45, Appl
C 580	6	0.8	71	4	US-08-963-851-16	Sequence 16, Appl	C 653	6	0.8	92	2	US-08-273-146-53	Sequence 53, Appl
C 581	6	0.8	71	4	US-09-904-615-152	Sequence 152, Appl	C 654	6	0.8	93	4	US-09-690-454-145	Sequence 145, Appl
C 582	6	0.8	71	4	US-09-107-532A-3721	Sequence 3721, Ap	C 655	6	0.8	93	4	US-09-252-991A-17144	Sequence 17144, A
C 583	6	0.8	72	4	US-08-469-260A-453	Sequence 453, Appl	C 656	6	0.8	94	4	US-09-107-532A-6511	Sequence 6511, Ap
C 584	6	0.8	72	4	US-09-252-991A-17145	Sequence 17145, A	C 657	6	0.8	95	3	US-08-928-383B-17	Sequence 17, Appl
C 585	6	0.8	72	4	US-08-488-446-453	Sequence 453, Appl	C 658	6	0.8	96	1	US-08-167-035-41	Sequence 41, Appl
C 586	6	0.8	72	4	US-08-467-344A-453	Sequence 453, Appl	C 659	6	0.8	96	1	US-08-208-887A-41	Sequence 41, Appl
C 587	6	0.8	73	1	US-08-379-538-7	Sequence 7, Appl	C 660	6	0.8	96	2	US-08-767-026-9	Sequence 9, Appl
C 588	6	0.8	73	4	US-08-469-260A-36	Sequence 36, Appl	C 661	6	0.8	96	2	US-08-539-005-41	Sequence 41, Appl
C 589	6	0.8	73	4	US-09-250-609-19	Sequence 19, Appl	C 662	6	0.8	96	2	US-08-737-560A-9	Sequence 9, Appl
C 590	6	0.8	73	4	US-09-611-19	Sequence 19, Appl	C 663	6	0.8	96	3	US-08-465-343A-11	Sequence 11, Appl
C 591	6	0.8	73	4	US-08-488-446-36	Sequence 36, Appl	C 664	6	0.8	96	4	US-09-280-598-38	Sequence 38, Appl
C 592	6	0.8	73	4	US-08-467-344A-36	Sequence 36, Appl	C 665	6	0.8	96	5	PCT-US93-08744-4	Sequence 4, Appl
C 593	6	0.8	74	3	US-09-177-249-56	Sequence 56, Appl	C 666	6	0.8	97	2	US-08-479-078-2	Sequence 2, Appl
C 594	6	0.8	74	4	US-09-227-357-265	Sequence 265, Appl	C 667	6	0.8	97	2	US-09-010-928B-21	Sequence 21, Appl
C 595	6	0.8	74	4	US-09-227-357-631	Sequence 631, Appl	C 668	6	0.8	97	4	US-09-205-258-699	Sequence 699, Ap
C 596	6	0.8	74	4	US-09-252-991A-17413	Sequence 17413, A	C 669	6	0.8	97	4	US-09-252-991A-32315	Sequence 32315, A

C 670	98	2	US-08-479-078-3	Sequence 3, Appli	C 743	6	0.8	114	4	US-09-252-991A-20170	Sequence 20170, A
C 671	98	2	US-08-479-078-4	Sequence 4, Appli	C 744	6	0.8	114	4	US-09-252-991A-21883	Sequence 21883, A
C 672	98	2	US-08-825-556A-4	Sequence 4, Appli	C 745	6	0.8	115	4	US-09-252-991A-27427	Sequence 27427, A
C 673	98	2	US-08-713-636-5	Sequence 5, Appli	C 746	6	0.8	115	4	US-09-732-210-662	Sequence 662, App
C 674	98	4	US-09-134-001C-3864	Sequence 3864, Ap	C 747	6	0.8	115	4	US-09-732-210-662	Sequence 982, App
C 675	98	4	US-09-238-184-4	Sequence 4, Appli	C 748	6	0.8	116	4	US-09-056-556-198	Sequence 198, App
C 676	99	1	US-08-202-389-35	Sequence 35, Appl	C 749	6	0.8	116	4	US-09-072-596-193	Sequence 193, App
C 677	99	1	US-08-202-389-36	Sequence 36, Appl	C 750	6	0.8	116	4	US-09-198-452A-289	Sequence 289, App
C 678	99	1	US-08-202-389-37	Sequence 37, Appl	C 751	6	0.8	117	1	US-08-499-215-3	Sequence 3, Appli
C 679	99	1	US-08-036-210-26	Sequence 26, Appl	C 752	6	0.8	118	4	US-09-134-001C-4334	Sequence 4334, Ap
C 680	99	2	US-08-449-609-26	Sequence 26, Appl	C 753	6	0.8	119	1	US-07-634-278-65	Sequence 65, Appl
C 681	99	4	US-09-227-357-630	Sequence 630, App	C 754	6	0.8	119	1	US-07-634-278-89	Sequence 89, Appl
C 682	99	4	US-09-361-096A-26	Sequence 26, Appl	C 755	6	0.8	119	1	US-08-477-728-65	Sequence 65, Appl
C 683	100	3	US-08-818-113-67	Sequence 4, Appli	C 756	6	0.8	119	1	US-08-477-728-89	Sequence 89, Appl
C 684	100	3	US-08-818-113-67	Sequence 67, Appl	C 757	6	0.8	119	1	US-08-474-040-85	Sequence 85, Appl
C 685	100	4	US-08-679-493A-146	Sequence 146, App	C 758	6	0.8	119	1	US-08-474-040-89	Sequence 89, Appl
C 686	100	4	US-08-818-111-68	Sequence 68, Appl	C 759	6	0.8	119	1	US-08-487-200-65	Sequence 65, Appl
C 687	100	4	US-09-056-556-67	Sequence 67, Appl	C 760	6	0.8	119	1	US-08-487-200-89	Sequence 89, Appl
C 688	100	4	US-09-072-596-68	Sequence 68, Appl	C 761	6	0.8	119	1	US-08-484-537-65	Sequence 65, Appl
C 689	100	4	US-09-482-273-142	Sequence 142, App	C 762	6	0.8	119	3	US-08-484-537-89	Sequence 89, Appl
C 690	101	4	US-09-107-532A-7251	Sequence 7251, Ap	C 763	6	0.8	119	4	US-09-252-991A-29926	Sequence 29926, A
C 691	101	4	US-09-199-637A-289	Sequence 289, App	C 764	6	0.8	119	4	US-09-328-352-7943	Sequence 7943, Ap
C 692	102	4	US-09-198-452A-475	Sequence 475, App	C 765	6	0.8	120	4	US-08-936-165A-357	Sequence 357, App
C 693	102	4	US-09-107-532A-6331	Sequence 6331, Ap	C 766	6	0.8	120	4	US-09-732-210-666	Sequence 666, App
C 694	103	4	US-09-252-991A-33050	Sequence 33050, A	C 767	6	0.8	121	4	US-09-252-991A-20801	Sequence 20801, A
C 695	104	4	US-09-732-210-987	Sequence 987, App	C 768	6	0.8	121	4	US-09-252-991A-27340	Sequence 27340, A
C 696	104	4	US-09-732-210-991	Sequence 991, App	C 769	6	0.8	122	1	US-07-634-278-88	Sequence 88, Appl
C 697	105	2	US-08-918-727-6	Sequence 6, Appli	C 770	6	0.8	122	1	US-08-477-728-88	Sequence 88, Appl
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## ALIGNMENTS

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RESULT 1
US-09-073-362-1
; Sequence 1, Application US/09073362
; Patent No. 5942399
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; REGISTRATION NUMBER: 39,132
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; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ESOGTUT02
; CLONE: 2667831
; US-09-073-362-1
; Alignment Scores:
; Pred. No.: 0.00317 Length: 511
; Score: 12.00 Matches: 12
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 1.64% Indels: 0
; DB: 2 Gaps: 0
; US-09-667-170A-440 (1-2239) x US-09-073-362-1 (1-511)
Qy 517 TAGCTGAATGGGAACAACACTATAAGAAATCTGGA 552
Db 90 TyrAlaGluLeuGlyThrThrLeLysSerGly 101
RESULT 2
US-09-243-920-1
; Sequence 1, Application US/09243920
; Patent No. 5981242
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/243,920
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/073,362
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0514 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid

```

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/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: ESOGTUT02
/ CLONE: 2667831
US-09-243-920-1
Alignment Scores:
Pred. No.: 0.00317 Length: 511
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.64% Indels: 0
DB: 2 Gaps: 0
US-09-667-170A-440 (1-2239) x US-09-243-920-1 (1-511)
QY 517 TAGCTGAATGGGAACAACATATAAAGAAATCTCGA 552
Db 90 TyrAlaGluLeuGlyThrThrIleLysLysSerGly 101
RESULT 3
US-09-732-210-157
/ Sequence 157, Application US/09732210
/ Patent No. 6573361
/ GENERAL INFORMATION:
/ APPLICANT: Bunkers, Greg J.
/ APPLICANT: Liang, Jihong
/ APPLICANT: Mittanck, Cindy A.
/ APPLICANT: Seale, Jeffrey W.
/ APPLICANT: Wu, Yonnie S.
/ TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
/ FILE REFERENCE: 38-21(15036)B
/ CURRENT APPLICATION NUMBER: US/09/732,210
/ CURRENT FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: US 60/169,513
/ PRIOR FILING DATE: 1999-12-07
/ PRIOR APPLICATION NUMBER: US 60/169,340
/ PRIOR FILING DATE: 1999-12-07
/ NUMBER OF SEQ ID NOS: 1753
/ SEQ ID NO 157
/ LENGTH: 67
/ TYPE: PRT
/ ORGANISM: Aquifex aeolicus
US-09-732-210-157
Alignment Scores:
Pred. No.: 36.4 Length: 67
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.09% Indels: 0
DB: 4 Gaps: 0
US-09-667-170A-440 (1-2239) x US-09-732-210-157 (1-67)
QY 77 GAAAGAAAGAAAAGAGAGAGAGG 100
Db 43 GluArgLysLysLysArgGluArg 50
RESULT 4
US-09-071-035-308
/ Sequence 308, Application US/09071035
/ Patent No. 6448043
/ GENERAL INFORMATION:
/ APPLICANT: Gil H. Choi
/ TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
/ NUMBER OF SEQUENCES: 496
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
```

```
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/071,035
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: A. Anders Brookes
/ REGISTRATION NUMBER: 36,373
/ REFERENCE/DOCKET NUMBER: PB369P2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 308:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 241 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-071-035-308
Alignment Scores:
Pred. No.: 31.3 Length: 241
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 4 Gaps: 0
US-09-667-170A-440 (1-2239) x US-09-071-035-308 (1-241)
QY 437 AGCAGCCCTTAGGAGAGATGAAG 414
Db 96 SerThrProLeuGlyGluMetLys 103
RESULT 5
US-09-071-035-306
/ Sequence 306, Application US/09071035
/ Patent No. 6448043
/ GENERAL INFORMATION:
/ APPLICANT: Gil H. Choi
/ TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
/ NUMBER OF SEQUENCES: 496
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/071,035
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: A. Anders Brookes
```

```
;
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 306:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-071-035-306

Alignment Scores:
Pred. No.: 30.8 Length: 275
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 4 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-071-035-306 (1-275)

QY 437 AGCAGCCCTTAGGAGATGAAG 414
Db 125 SerThrProLeuGlyMetLys 132

RESULT 6
US-09-198-452A-405
; Sequence 405, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 405
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...325
; OTHER INFORMATION: Xaa-unknown or other
US-09-198-452A-405

Alignment Scores:
Pred. No.: 30.2 Length: 325
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 4 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-198-452A-405 (1-325)

QY 380 GAGACTCCCTCAGTAAGTACT 357
Db 149 GluThrProLeuSerLysValThr 156

RESULT 7
US-09-328-352-6531
; Sequence 6531, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6531
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-6531

Alignment Scores:
Pred. No.: 30.1 Length: 332
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 4 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-328-352-6531 (1-332)

QY 1717 CTGTACAACTTCCAGTATTATT 1694
Db 30 LeuValGlnLeuProValLeuPhe 37

RESULT 8
US-09-073-362-3
; Sequence 3, Application US/09073362
; Patent No. 5942399
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Carrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0514 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1665759
US-09-073-362-3

Alignment Scores:
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Pred. No.: 28.6 Length: 515  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.09% Indels: 0  
DB: 2 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-073-362-3 (1-515)

QY 517 TATGCTGAATGGGAACAATA 540

Db 98 TyrAlaGluLeuGlyThrThrile 105

RESULT 9

US-09-243-920-3  
; Sequence 3, Application US/09243920  
; Patent No. 5981242  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/243,920  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA: 09/073,362

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0514 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 515 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 1665759

US-09-243-920-3

Alignment Scores:

Pred. No.: 28.6 Length: 515  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.09% Indels: 0  
DB: 2 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-243-920-3 (1-515)

QY 517 TATGCTGAATGGGAACAATA 540

Db 98 TyrAlaGluLeuGlyThrThrile 105

Db 98 TyrAlaGluLeuGlyThrThrile 105

RESULT 10

US-09-107-532A-4126

; Sequence 4126, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4126:

SEQUENCE CHARACTERISTICS:

LENGTH: 585 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...585

SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

US-09-107-532A-4126

Alignment Scores:

Pred. No.: 28.2 Length: 585  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.12% Indels: 0  
DB: 4 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-107-532A-4126 (1-585)

QY 90 TTTTCTCTCTCTCTCTCTCTCT 67

Db 175 PhePhePheLeuSerPhePheLeu 182

RESULT 11

US-09-252-991A-19955

; Sequence 19955, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.



1 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
2 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
3 FILE REFERENCE: 107196.136

4 CURRENT APPLICATION NUMBER: US/09/252,991A

5 CURRENT FILING DATE: 1998-02-18

6 PRIOR APPLICATION NUMBER: US 60/074,788

7 PRIOR FILING DATE: 1998-02-18

8 PRIOR APPLICATION NUMBER: US 60/094,190

9 PRIOR FILING DATE: 1998-07-27

10 NUMBER OF SEQ ID NOS: 33142

11 SEQ ID NO 19955

12 LENGTH: 613

13 TYPE: PRT

14 ORGANISM: Pseudomonas aeruginosa

15 US-09-252-991A-19955

Alignment Scores:

Pred. No.:	28	Length:	613
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.09%	Indels:	0
DB:	4	Gaps:	0

US-09-667-170A-440 (1-2239) x US-09-252-991A-19955 (1-613)

Qy 434 TGCTCCAGACACGGCGCGTGG 457

Db 27 CysSerArgThrGalaalaTTP 34

RESULT 12

US-09-012-710-11

Sequence 11, Application US/09012710

Patent No. 6087478

GENERAL INFORMATION:

APPLICANT: Vinkemeier, Uwe

APPLICANT: Moarefi, Ismail

APPLICANT: Darneil, Jr., James E.

APPLICANT: Kuriyan, John

TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A

TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/012,710

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-194

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 786 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

1 HYPOTHETICAL: NO

US-09-012-710-11

Alignment Scores:

Pred. No.:	27.2	Length:	786
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.09%	Indels:	0
DB:	3	Gaps:	0

US-09-667-170A-440 (1-2239) x US-09-012-710-11 (1-786)

Qy 766 AATAGCATGATGTCACCTGAGC 789

Db 549 AsnSerMetSerValSerTTPSer 556

RESULT 13

US-09-556-273-11

Sequence 11, Application US/09556273

Patent No. 6312887

GENERAL INFORMATION:

APPLICANT: Vinkemeier, Uwe

APPLICANT: Moarefi, Ismail

APPLICANT: Darneil, Jr., James E.

APPLICANT: Kuriyan, John

TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A

TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/556,273

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/012,710

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-194

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 786 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

US-09-556-273-11

Alignment Scores:

Pred. No.:	27.2	Length:	786
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.09%	Indels:	0
DB:	4	Gaps:	0

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US-09-667-170A-440 (1-2239) x US-09-556-273-11 (1-786)
QY 766 AATAGCATGAGTGTGAGCTGGAGC 789
Db 549 AsnSerMetSerValSerTyrSer 556

RESULT 14
US-09-012-710-10
; Sequence 10, Application US/09012710
; Patent No. 6087478
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-012-710-10

Alignment Scores:
Pred. No.: 27.2 Length: 793
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.09% Indels: 0
DB: 3 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-012-710-10 (1-793)
QY 766 AATAGCATGAGTGTGAGCTGGAGC 789
Db 549 AsnSerMetSerValSerTyrSer 556

RESULT 15
US-09-556-273-10
; Sequence 10, Application US/09556273
; Patent No. 6312887
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
```

```
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/556,273
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-556-273-10

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.09% Indels: 0
DB: 4 Gaps: 0

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Db 549 AsnSerMetSerValSerTyrSer 556

Search completed: October 31, 2003, 11:56:36
Job time : 73 secs
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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_r2p model

Run on: October 31, 2003, 11:53:22 ; Search time 141 Seconds

(without alignments)  
5435.405 Million cell updates/sec

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Perfect score: 732

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Searched: 642050 seqs, 171146064 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1213976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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227	8	1.1	594	12	US-10-152-377-10	Sequence 10, Appl	300	8	1.1	594	15	US-10-131-823A-10	Sequence 10, Appl
228	8	1.1	594	12	US-10-152-386-10	Sequence 10, Appl	301	8	1.1	594	15	US-10-131-823A-10	Sequence 10, Appl
229	8	1.1	594	12	US-10-152-391-10	Sequence 10, Appl	302	8	1.1	594	15	US-10-131-824A-10	Sequence 10, Appl
230	8	1.1	594	12	US-10-152-393-10	Sequence 10, Appl	303	8	1.1	594	15	US-10-131-830A-10	Sequence 10, Appl
231	8	1.1	594	12	US-10-156-848-10	Sequence 10, Appl	304	8	1.1	594	15	US-10-131-837A-10	Sequence 10, Appl
232	8	1.1	594	12	US-10-157-785-10	Sequence 10, Appl	305	8	1.1	594	15	US-10-137-872A-10	Sequence 10, Appl
233	8	1.1	594	12	US-10-157-794-10	Sequence 10, Appl	306	8	1.1	594	15	US-10-147-500-10	Sequence 10, Appl
234	8	1.1	594	12	US-10-157-796-10	Sequence 10, Appl	307	8	1.1	594	15	US-10-147-502-10	Sequence 10, Appl
235	8	1.1	594	12	US-10-160-500-10	Sequence 10, Appl	308	8	1.1	594	15	US-10-147-515-10	Sequence 10, Appl
236	8	1.1	594	12	US-10-121-048-10	Sequence 10, Appl	309	8	1.1	594	15	US-10-147-517-10	Sequence 10, Appl
237	8	1.1	594	12	US-10-121-052-10	Sequence 10, Appl	310	8	1.1	594	15	US-10-147-526-10	Sequence 10, Appl
238	8	1.1	594	12	US-10-121-053-10	Sequence 10, Appl	311	8	1.1	594	15	US-10-147-527-10	Sequence 10, Appl
239	8	1.1	594	12	US-10-121-054-10	Sequence 10, Appl	312	8	1.1	594	15	US-10-121-041-10	Sequence 10, Appl
240	8	1.1	594	12	US-10-121-063-10	Sequence 10, Appl	313	8	1.1	594	15	US-10-121-043-10	Sequence 10, Appl
241	8	1.1	594	12	US-10-123-212-10	Sequence 10, Appl	314	8	1.1	594	15	US-10-121-047-10	Sequence 10, Appl
242	8	1.1	594	12	US-10-123-213-10	Sequence 10, Appl	315	8	1.1	594	15	US-10-123-215-10	Sequence 10, Appl
243	8	1.1	594	12	US-10-123-251-10	Sequence 10, Appl	316	8	1.1	594	15	US-10-123-902-10	Sequence 10, Appl
244	8	1.1	594	12	US-10-123-322-10	Sequence 10, Appl	317	8	1.1	594	15	US-10-123-908-10	Sequence 10, Appl
245	8	1.1	594	12	US-10-123-771-10	Sequence 10, Appl	318	8	1.1	594	15	US-10-123-909-10	Sequence 10, Appl
246	8	1.1	594	12	US-10-123-911-10	Sequence 10, Appl	319	8	1.1	594	15	US-10-123-910-10	Sequence 10, Appl
247	8	1.1	594	12	US-10-124-821-10	Sequence 10, Appl	320	8	1.1	594	15	US-10-124-813-10	Sequence 10, Appl
248	8	1.1	594	12	US-10-124-823-10	Sequence 10, Appl	321	8	1.1	594	15	US-10-124-817-10	Sequence 10, Appl
249	8	1.1	594	12	US-10-125-931-10	Sequence 10, Appl	322	8	1.1	594	15	US-10-125-922-10	Sequence 10, Appl
250	8	1.1	594	12	US-10-125-932-10	Sequence 10, Appl	323	8	1.1	594	15	US-10-125-924-10	Sequence 10, Appl
251	8	1.1	594	12	US-10-125-385-10	Sequence 10, Appl	324	8	1.1	594	15	US-10-140-860-10	Sequence 10, Appl
252	8	1.1	594	12	US-10-152-393-10	Sequence 10, Appl	325	8	1.1	594	15	US-10-142-417-10	Sequence 10, Appl
253	8	1.1	594	12	US-10-152-396-10	Sequence 10, Appl	326	8	1.1	594	15	US-10-147-519-10	Sequence 10, Appl
254	8	1.1	594	12	US-10-153-552-10	Sequence 10, Appl	327	8	1.1	594	15	US-10-157-782-10	Sequence 10, Appl
255	8	1.1	594	12	US-10-153-840-10	Sequence 10, Appl	328	8	1.1	594	15	US-10-152-395-10	Sequence 10, Appl
256	8	1.1	594	12	US-10-156-841-10	Sequence 10, Appl	329	8	1.1	594	15	US-10-125-926A-10	Sequence 10, Appl
257	8	1.1	594	12	US-10-156-842-10	Sequence 10, Appl	330	8	1.1	594	15	US-10-125-930A-10	Sequence 10, Appl
258	8	1.1	594	12	US-10-156-844-10	Sequence 10, Appl	331	8	1.1	594	15	US-10-127-831A-10	Sequence 10, Appl
259	8	1.1	594	12	US-10-156-845-10	Sequence 10, Appl	332	8	1.1	594	15	US-10-127-837A-10	Sequence 10, Appl
260	8	1.1	594	12	US-10-156-846-10	Sequence 10, Appl	333	8	1.1	594	15	US-10-127-838B-10	Sequence 10, Appl
261	8	1.1	594	15	US-10-028-072-10	Sequence 10, Appl	334	8	1.1	594	15	US-10-127-842A-10	Sequence 10, Appl
262	8	1.1	594	15	US-10-121-049-10	Sequence 10, Appl	335	8	1.1	594	15	US-10-127-843A-10	Sequence 10, Appl
263	8	1.1	594	15	US-10-123-904-10	Sequence 10, Appl	336	8	1.1	594	15	US-10-127-845A-10	Sequence 10, Appl
264	8	1.1	594	15	US-10-140-470-10	Sequence 10, Appl	337	8	1.1	594	15	US-10-127-846A-10	Sequence 10, Appl
265	8	1.1	594	15	US-10-175-746-10	Sequence 10, Appl	338	8	1.1	594	15	US-10-127-848A-10	Sequence 10, Appl
266	8	1.1	594	15	US-10-176-918-10	Sequence 10, Appl	339	8	1.1	594	15	US-10-127-849A-10	Sequence 10, Appl
267	8	1.1	594	15	US-10-176-921-10	Sequence 10, Appl	340	8	1.1	594	15	US-10-127-850A-10	Sequence 10, Appl
268	8	1.1	594	15	US-10-137-865-10	Sequence 10, Appl	341	8	1.1	594	15	US-10-127-851A-10	Sequence 10, Appl
269	8	1.1	594	15	US-10-140-471-10	Sequence 10, Appl	342	8	1.1	594	15	US-10-128-684A-10	Sequence 10, Appl
270	8	1.1	594	15	US-10-142-431-10	Sequence 10, Appl	343	8	1.1	594	15	US-10-128-686A-10	Sequence 10, Appl
271	8	1.1	594	15	US-10-143-114-10	Sequence 10, Appl	344	8	1.1	594	15	US-10-128-690A-10	Sequence 10, Appl
272	8	1.1	594	15	US-10-140-002-10	Sequence 10, Appl	345	8	1.1	594	15	US-10-128-691A-10	Sequence 10, Appl
273	8	1.1	594	15	US-10-142-419-10	Sequence 10, Appl	346	8	1.1	594	15	US-10-131-819A-10	Sequence 10, Appl
274	8	1.1	594	15	US-10-123-262-10	Sequence 10, Appl	347	8	1.1	594	15	US-10-131-829A-10	Sequence 10, Appl
275	8	1.1	594	15	US-10-142-423-10	Sequence 10, Appl	348	8	1.1	594	15	US-10-146-729-10	Sequence 10, Appl
276	8	1.1	594	15	US-10-121-050-10	Sequence 10, Appl	349	8	1.1	594	15	US-10-146-791-10	Sequence 10, Appl
277	8	1.1	594	15	US-10-141-755-10	Sequence 10, Appl	350	8	1.1	594	15	US-10-147-484-10	Sequence 10, Appl
278	8	1.1	594	15	US-10-143-032-10	Sequence 10, Appl	351	8	1.1	594	15	US-10-147-508-10	Sequence 10, Appl
279	8	1.1	594	15	US-10-123-236-10	Sequence 10, Appl	352	8	1.1	594	15	US-10-147-512-10	Sequence 10, Appl
280	8	1.1	594	15	US-10-123-261-10	Sequence 10, Appl	353	8	1.1	594	15	US-10-175-735-10	Sequence 10, Appl
281	8	1.1	594	15	US-10-140-921-10	Sequence 10, Appl	354	8	1.1	594	15	US-10-121-040-10	Sequence 10, Appl
282	8	1.1	594	15	US-10-140-928-10	Sequence 10, Appl	355	8	1.1	594	15	US-10-121-056-10	Sequence 10, Appl
283	8	1.1	594	15	US-10-121-045-10	Sequence 10, Appl	356	8	1.1	594	15	US-10-121-061-10	Sequence 10, Appl
284	8	1.1	594	15	US-10-123-292-10	Sequence 10, Appl	357	8	1.1	594	15	US-10-123-235-10	Sequence 10, Appl
285	8	1.1	594	15	US-10-123-903-10	Sequence 10, Appl	358	8	1.1	594	15	US-10-124-818-10	Sequence 10, Appl
286	8	1.1	594	15	US-10-124-819-10	Sequence 10, Appl	359	8	1.1	594	15	US-10-137-868-10	Sequence 10, Appl
287	8	1.1	594	15	US-10-124-809-10	Sequence 10, Appl	360	8	1.1	594	15	US-10-147-492-10	Sequence 10, Appl
288	8	1.1	594	15	US-10-124-822-10	Sequence 10, Appl	361	8	1.1	594	15	US-10-158-782-10	Sequence 10, Appl
289	8	1.1	594	15	US-10-140-925-10	Sequence 10, Appl	362	8	1.1	594	15	US-10-123-905-10	Sequence 10, Appl
290	8	1.1	594	15	US-10-160-498-10	Sequence 10, Appl	363	8	1.1	594	15	US-10-123-907-10	Sequence 10, Appl
291	8	1.1	594	15	US-10-124-824-10	Sequence 10, Appl	364	8	1.1	594	15	US-10-124-815-10	Sequence 10, Appl
292	8	1.1	594	15	US-10-127-825A-10	Sequence 10, Appl	365	8	1.1	594	15	US-10-125-921A-10	Sequence 10, Appl

366	8	1.1	594	15	US-10-125-928A-10	Sequence 10, Appl	C 439	7	1.0	30	15	US-10-083-357-937	Sequence 937, App
367	8	1.1	594	15	US-10-127-821A-10	Sequence 10, Appl	440	7	1.0	31	9	US-09-864-761-38137	Sequence 38137, A
368	8	1.1	594	15	US-10-127-822A-10	Sequence 10, Appl	441	7	1.0	31	9	US-09-864-761-42737	Sequence 42737, A
369	8	1.1	594	15	US-10-127-824A-10	Sequence 10, Appl	C 442	7	1.0	34	10	US-09-764-877-1187	Sequence 1187, App
370	8	1.1	594	15	US-10-127-826A-10	Sequence 10, Appl	443	7	1.0	34	10	US-09-764-872-359	Sequence 359, App
371	8	1.1	594	15	US-10-127-827A-10	Sequence 10, Appl	444	7	1.0	37	11	US-09-764-872-359	Sequence 1018, App
372	8	1.1	594	15	US-10-127-828A-10	Sequence 10, Appl	445	7	1.0	47	15	US-09-764-869-1018	Sequence 1018, App
373	8	1.1	594	15	US-10-127-830A-10	Sequence 10, Appl	446	7	1.0	47	15	US-10-091-504-1018	Sequence 1018, App
374	8	1.1	594	15	US-10-127-832A-10	Sequence 10, Appl	447	7	1.0	47	15	US-10-050-882-155	Sequence 155, App
375	8	1.1	594	15	US-10-127-833A-10	Sequence 10, Appl	C 447	7	1.0	48	15	US-10-097-065-193	Sequence 193, App
376	8	1.1	594	15	US-10-127-834A-10	Sequence 10, Appl	C 448	7	1.0	55	9	US-09-864-761-37143	Sequence 37143, A
377	8	1.1	594	15	US-10-127-836A-10	Sequence 10, Appl	C 449	7	1.0	56	10	US-09-995-494-109	Sequence 109, App
378	8	1.1	594	15	US-10-127-841A-10	Sequence 10, Appl	450	7	1.0	58	10	US-09-796-692-1489	Sequence 1489, App
379	8	1.1	594	15	US-10-127-844A-10	Sequence 10, Appl	451	7	1.0	58	10	US-10-040-862-1489	Sequence 203, App
380	8	1.1	594	15	US-10-128-687A-10	Sequence 10, Appl	C 452	7	1.0	61	10	US-09-764-887-203	Sequence 203, App
381	8	1.1	594	15	US-10-128-688A-10	Sequence 10, Appl	453	7	1.0	61	10	US-09-796-692-1082	Sequence 1082, App
382	8	1.1	594	15	US-10-128-689A-10	Sequence 10, Appl	454	7	1.0	61	10	US-09-796-692-1556	Sequence 1556, App
383	8	1.1	594	15	US-10-128-690A-10	Sequence 10, Appl	455	7	1.0	61	10	US-09-796-692-1953	Sequence 1953, App
384	8	1.1	594	15	US-10-128-691A-10	Sequence 10, Appl	456	7	1.0	61	10	US-09-796-692-2192	Sequence 2192, App
385	8	1.1	594	15	US-10-131-825A-10	Sequence 10, Appl	C 457	7	1.0	61	15	US-10-073-561-203	Sequence 203, App
386	8	1.1	594	15	US-10-230-417-10	Sequence 10, Appl	458	7	1.0	61	15	US-10-040-862-1082	Sequence 1082, App
387	8	1.1	594	15	US-10-131-815A-10	Sequence 10, Appl	459	7	1.0	61	15	US-10-040-862-1556	Sequence 1556, App
388	8	1.1	594	15	US-10-131-817A-10	Sequence 10, Appl	460	7	1.0	61	15	US-10-040-862-1556	Sequence 1556, App
389	8	1.1	594	15	US-10-131-822A-10	Sequence 10, Appl	461	7	1.0	61	15	US-10-040-862-1556	Sequence 1556, App
390	8	1.1	594	15	US-10-131-828A-10	Sequence 10, Appl	C 462	7	1.0	61	15	US-10-040-862-1556	Sequence 1556, App
391	8	1.1	594	15	US-10-131-835A-10	Sequence 10, Appl	C 463	7	1.0	61	15	US-10-040-862-1556	Sequence 1556, App
392	8	1.1	594	15	US-10-137-864A-10	Sequence 10, Appl	464	7	1.0	61	15	US-10-040-862-1556	Sequence 1556, App
393	8	1.1	594	15	US-10-137-869A-10	Sequence 10, Appl	465	7	1.0	63	9	US-09-867-550-870	Sequence 5140, App
394	8	1.1	594	15	US-10-137-875A-10	Sequence 10, Appl	466	7	1.0	63	14	US-10-117-604-2	Sequence 870, App
395	8	1.1	594	15	US-10-138-785-10	Sequence 10, Appl	C 467	7	1.0	66	10	US-09-764-877-1089	Sequence 2, Appl1
396	8	1.1	594	15	US-10-121-051-10	Sequence 10, Appl	C 468	7	1.0	67	11	US-09-764-891-4662	Sequence 1089, App
397	8	1.1	594	15	US-10-121-042-10	Sequence 10, Appl	C 469	7	1.0	69	10	US-09-796-692-2308	Sequence 4682, App
398	8	1.1	594	15	US-10-123-912-10	Sequence 10, Appl	C 470	7	1.0	69	15	US-09-796-692-2308	Sequence 2308, App
399	8	1.1	594	15	US-10-132-007-10	Sequence 10, Appl	471	7	1.0	71	9	US-09-925-297-565	Sequence 2308, App
400	8	1.1	594	15	US-10-134-359-10	Sequence 10, Appl	472	7	1.0	74	9	US-09-925-302-509	Sequence 565, App
401	8	1.1	594	15	US-10-175-590-10	Sequence 10, Appl	C 473	7	1.0	74	9	US-09-864-761-47086	Sequence 509, App
402	8	1.1	594	15	US-10-175-590-10	Sequence 10, Appl	474	7	1.0	76	14	US-10-002-344A-223	Sequence 47086, A
403	8	1.1	594	16	US-10-137-866-10	Sequence 10, Appl	C 475	7	1.0	77	10	US-09-989-919-97	Sequence 229, App
404	8	1.1	594	16	US-10-146-726-10	Sequence 10, Appl	C 476	7	1.0	78	9	US-09-864-761-39418	Sequence 97, Appl1
405	8	1.1	594	16	US-10-146-727-10	Sequence 10, Appl	C 477	7	1.0	79	12	US-10-238-075-1451	Sequence 39418, A
406	8	1.1	594	16	US-10-146-788-10	Sequence 10, Appl	478	7	1.0	83	9	US-09-925-301-1468	Sequence 1451, App
407	8	1.1	594	16	US-10-152-380-10	Sequence 10, Appl	C 479	7	1.0	85	10	US-09-731-873-307	Sequence 1468, App
408	8	1.1	594	16	US-10-153-834-10	Sequence 10, Appl	480	7	1.0	85	11	US-09-764-891-4758	Sequence 307, App
409	8	1.1	786	15	US-10-045-792-11	Sequence 11, Appl	481	7	1.0	85	12	US-09-876-997-307	Sequence 4758, App
410	8	1.1	793	15	US-10-045-792-10	Sequence 10, Appl	482	7	1.0	86	9	US-09-864-761-34118	Sequence 307, App
411	8	1.1	2227	10	US-09-929-955-12	Sequence 12, Appl	483	7	1.0	86	10	US-09-731-873-290	Sequence 34118, A
412	8	1.1	2227	14	US-10-104-566-12	Sequence 12, Appl	C 484	7	1.0	86	12	US-09-876-997-290	Sequence 290, App
413	8	1.1	2227	14	US-10-135-988-2	Sequence 2, Appl	485	7	1.0	87	9	US-09-864-761-39625	Sequence 290, App
414	8	1.1	2227	14	US-10-135-988-4	Sequence 4, Appl1	486	7	1.0	87	10	US-09-764-878-151	Sequence 39625, A
415	8	1.1	2227	14	US-10-135-988-6	Sequence 6, Appl1	487	7	1.0	87	11	US-09-764-891-2986	Sequence 151, App
416	8	1.1	10	11	US-09-572-404B-2392	Sequence 2392, App	C 488	7	1.0	87	15	US-10-079-854-151	Sequence 151, App
417	7	1.0	10	11	US-09-572-404B-2394	Sequence 2394, App	489	7	1.0	87	15	US-10-091-572-329	Sequence 329, App
418	7	1.0	17	10	US-09-791-378-122	Sequence 122, App	490	7	1.0	89	11	US-09-764-891-3854	Sequence 3854, App
419	7	1.0	22	11	US-09-865-989-156	Sequence 156, App	491	7	1.0	93	9	US-09-864-761-36529	Sequence 36529, A
420	7	1.0	22	11	US-09-865-989-156	Sequence 156, App	492	7	1.0	93	9	US-09-864-761-46910	Sequence 46910, A
421	7	1.0	22	11	US-09-865-989-156	Sequence 156, App	C 493	7	1.0	94	11	US-09-866-050A-676	Sequence 676, App
422	7	1.0	22	11	US-09-865-989-166	Sequence 166, App	C 494	7	1.0	95	10	US-09-864-761-48467	Sequence 48467, A
423	7	1.0	22	11	US-09-865-989-172	Sequence 172, App	C 495	7	1.0	95	10	US-09-925-300-1736	Sequence 1736, App
424	7	1.0	22	11	US-09-865-989-177	Sequence 177, App	C 496	7	1.0	99	11	US-09-764-872-435	Sequence 435, App
425	7	1.0	22	11	US-09-865-989-184	Sequence 184, App	C 497	7	1.0	101	15	US-10-106-698-4733	Sequence 4733, App
426	7	1.0	22	12	US-10-147-849-156	Sequence 156, App	498	7	1.0	106	9	US-09-864-761-40902	Sequence 40902, A
427	7	1.0	22	12	US-10-147-849-166	Sequence 166, App	499	7	1.0	106	14	US-10-001-870-200	Sequence 200, App
428	7	1.0	22	12	US-10-147-849-172	Sequence 172, App	500	7	1.0	107	10	US-09-071-838-145	Sequence 145, App
429	7	1.0	22	12	US-10-147-849-177	Sequence 177, App	501	7	1.0	107	12	US-10-252-131-16	Sequence 16, Appl1
430	7	1.0	22	12	US-10-147-849-184	Sequence 184, App	502	7	1.0	107	15	US-10-004-633-16	Sequence 16, Appl1
431	7	1.0	22	12	US-10-147-849-184	Sequence 184, App	503	7	1.0	107	15	US-10-213-512-145	Sequence 145, App
432	7	1.0	22	15	US-10-099-574A-156	Sequence 156, App	504	7	1.0	110	12	US-10-253-131-15	Sequence 15, Appl1
433	7	1.0	22	15	US-10-099-574A-158	Sequence 158, App	505	7	1.0	110	15	US-10-004-633-15	Sequence 15, Appl1
434	7	1.0	22	15	US-10-099-574A-166	Sequence 166, App	C 507	7	1.0	112	12	US-10-342-224-38	Sequence 6857, App
435	7	1.0	22	15	US-10-099-574A-172	Sequence 172, App	C 508	7	1.0	115	15	US-10-007-280A-205	Sequence 205, Appl
436	7	1.0	22	15	US-10-099-574A-177	Sequence 177, App	509	7	1.0	117	9	US-09-864-761-43183	Sequence 43183, A
437	7	1.0	22	15	US-10-099-574A-184	Sequence 184, App	510	7	1.0	121	10	US-09-764-864-1125	Sequence 1125, App
438	7	1.0	25	11	US-09-983-802-624	Sequence 624, App	511	7	1.0	122	9	US-09-764-869-788	Sequence 788, App

c 512	7	1.0	122	15	US-10-091-504-788	Sequence 788, App	c 585	7	1.0	337	15	US-10-167-192-3	Sequence 3, Appli
c 513	7	1.0	123	14	US-10-001-857-177	Sequence 177, App	c 586	7	1.0	337	15	US-10-225-567A-547	Sequence 547, App
c 514	7	1.0	127	9	US-09-815-242-10432	Sequence 10432, A	c 587	7	1.0	337	15	US-10-290-078-21	Sequence 21, Appl
c 515	7	1.0	130	10	US-09-731-872-289	Sequence 289, App	c 588	7	1.0	340	15	US-10-156-761-13234	Sequence 13234, A
c 516	7	1.0	130	11	US-09-798-889-63	Sequence 63, Appl	c 589	7	1.0	346	12	US-10-032-585-7398	Sequence 7398, App
c 517	7	1.0	130	11	US-09-876-997-289	Sequence 289, App	c 590	7	1.0	350	12	US-10-112-356-7	Sequence 7, Appli
c 518	7	1.0	130	12	US-10-252-131-13	Sequence 13, Appl	c 591	7	1.0	350	15	US-10-225-567A-164	Sequence 164, App
c 519	7	1.0	130	12	US-10-252-131-14	Sequence 14, Appl	c 592	7	1.0	353	9	US-09-895-943-3	Sequence 3, Appli
c 520	7	1.0	130	15	US-10-004-633-13	Sequence 13, Appl	c 593	7	1.0	353	10	US-09-895-593-3	Sequence 3, Appli
c 521	7	1.0	130	15	US-10-004-633-14	Sequence 14, Appl	c 594	7	1.0	354	15	US-10-156-761-8704	Sequence 8704, App
c 522	7	1.0	130	15	US-10-471-311-73	Sequence 73, Appl	c 595	7	1.0	357	9	US-09-779-427-3	Sequence 3, Appli
c 523	7	1.0	130	15	US-10-177-293-170	Sequence 170, App	c 596	7	1.0	365	9	US-09-815-242-11917	Sequence 11917, A
c 524	7	1.0	131	12	US-10-195-730-141	Sequence 141, App	c 597	7	1.0	365	15	US-10-198-070-40	Sequence 40, Appl
c 525	7	1.0	133	11	US-09-764-872-338	Sequence 338, App	c 598	7	1.0	365	15	US-10-156-761-14079	Sequence 14079, A
c 526	7	1.0	133	15	US-10-198-070-45	Sequence 45, Appl	c 599	7	1.0	370	9	US-09-895-943-2	Sequence 2, Appli
c 527	7	1.0	135	10	US-09-764-877-1450	Sequence 1450, App	c 600	7	1.0	370	10	US-09-895-593-2	Sequence 2, Appli
c 528	7	1.0	135	10	US-09-860-670-132	Sequence 132, App	c 601	7	1.0	372	12	US-10-087-887-54	Sequence 54, Appl
c 529	7	1.0	138	15	US-10-176-847-12	Sequence 12, Appl	c 602	7	1.0	381	15	US-10-156-761-11111	Sequence 11111, A
c 530	7	1.0	143	9	US-09-736-959A-11	Sequence 11, Appl	c 603	7	1.0	390	10	US-09-895-913A-286	Sequence 286, App
c 531	7	1.0	150	12	US-10-017-161-1174	Sequence 1174, App	c 604	7	1.0	391	15	US-10-156-761-14719	Sequence 14719, A
c 532	7	1.0	150	12	US-10-017-161-1806	Sequence 1806, App	c 605	7	1.0	394	10	US-09-886-055-341	Sequence 341, App
c 533	7	1.0	155	14	US-10-001-835-213	Sequence 213, App	c 606	7	1.0	394	11	US-09-804-291-341	Sequence 341, App
c 534	7	1.0	157	12	US-10-017-161-1494	Sequence 1494, App	c 607	7	1.0	394	11	US-09-284-320-81	Sequence 81, Appl
c 535	7	1.0	157	12	US-10-017-161-1500	Sequence 1500, App	c 608	7	1.0	397	10	US-09-738-628-3831	Sequence 3831, App
c 536	7	1.0	157	16	US-10-174-693-341	Sequence 341, App	c 609	7	1.0	401	15	US-10-106-698-6192	Sequence 6192, App
c 537	7	1.0	158	12	US-10-017-161-1158	Sequence 1158, App	c 610	7	1.0	405	12	US-10-017-161-2256	Sequence 2256, App
c 538	7	1.0	158	12	US-10-017-161-1948	Sequence 1948, App	c 611	7	1.0	406	10	US-09-731-872-245	Sequence 245, App
c 539	7	1.0	161	9	US-09-736-959A-1	Sequence 1, Appli	c 612	7	1.0	406	12	US-10-137-870-66	Sequence 66, Appl
c 540	7	1.0	161	9	US-09-736-959A-32	Sequence 32, Appl	c 613	7	1.0	406	12	US-10-137-870-258	Sequence 258, App
c 541	7	1.0	165	9	US-09-938-970-6	Sequence 6, Appli	c 614	7	1.0	406	12	US-10-140-018-66	Sequence 66, Appl
c 542	7	1.0	165	12	US-10-029-386-32399	Sequence 32399, A	c 615	7	1.0	406	12	US-10-140-018-258	Sequence 258, App
c 543	7	1.0	168	12	US-10-017-161-1324	Sequence 1324, App	c 616	7	1.0	406	12	US-10-140-021-66	Sequence 66, Appl
c 544	7	1.0	170	10	US-09-764-868-816	Sequence 816, App	c 617	7	1.0	406	12	US-10-140-021-258	Sequence 258, App
c 545	7	1.0	172	12	US-10-017-161-1702	Sequence 1702, App	c 618	7	1.0	406	12	US-10-140-274-66	Sequence 66, Appl
c 546	7	1.0	178	11	US-09-798-889-114	Sequence 114, App	c 619	7	1.0	406	12	US-10-140-274-258	Sequence 258, App
c 547	7	1.0	180	9	US-08-811-284-132	Sequence 132, App	c 620	7	1.0	406	12	US-10-140-471-66	Sequence 66, Appl
c 548	7	1.0	181	9	US-09-942-446-6	Sequence 6, Appli	c 621	7	1.0	406	12	US-10-140-471-258	Sequence 258, App
c 549	7	1.0	181	15	US-10-156-761-10026	Sequence 10026, A	c 622	7	1.0	406	12	US-10-140-807-66	Sequence 66, Appl
c 550	7	1.0	182	15	US-10-295-732-3	Sequence 3, Appli	c 623	7	1.0	406	12	US-10-140-807-258	Sequence 258, App
c 551	7	1.0	189	12	US-10-017-161-1104	Sequence 1104, App	c 624	7	1.0	406	12	US-10-140-922-66	Sequence 66, Appl
c 552	7	1.0	192	15	US-10-021-811-50	Sequence 50, Appl	c 625	7	1.0	406	12	US-10-140-922-258	Sequence 258, App
c 553	7	1.0	193	12	US-10-022-6310-54	Sequence 54, Appl	c 626	7	1.0	406	12	US-10-140-924-66	Sequence 66, Appl
c 554	7	1.0	196	15	US-10-252-646-8	Sequence 8, Appli	c 627	7	1.0	406	12	US-10-140-924-258	Sequence 258, App
c 555	7	1.0	203	11	US-09-791-279-140	Sequence 140, App	c 628	7	1.0	406	12	US-10-140-926-66	Sequence 66, Appl
c 556	7	1.0	204	12	US-10-017-161-1502	Sequence 1502, App	c 629	7	1.0	406	12	US-10-140-926-258	Sequence 258, App
c 557	7	1.0	210	12	US-10-017-161-594	Sequence 594, App	c 630	7	1.0	406	12	US-10-141-698-66	Sequence 66, Appl
c 558	7	1.0	215	10	US-09-747-155-421	Sequence 421, App	c 631	7	1.0	406	12	US-10-141-698-258	Sequence 258, App
c 559	7	1.0	218	10	US-09-738-626-4999	Sequence 4999, App	c 632	7	1.0	406	12	US-10-141-702-66	Sequence 66, Appl
c 560	7	1.0	219	12	US-10-017-161-980	Sequence 980, App	c 633	7	1.0	406	12	US-10-141-702-258	Sequence 258, App
c 561	7	1.0	233	9	US-09-815-242-4966	Sequence 4966, App	c 634	7	1.0	406	12	US-10-141-704-66	Sequence 66, Appl
c 562	7	1.0	233	9	US-09-815-242-10829	Sequence 10829, A	c 635	7	1.0	406	12	US-10-141-704-258	Sequence 258, App
c 563	7	1.0	242	15	US-10-156-761-12298	Sequence 12298, A	c 636	7	1.0	406	12	US-10-142-421-66	Sequence 66, Appl
c 564	7	1.0	264	10	US-09-738-626-4518	Sequence 4518, App	c 637	7	1.0	406	12	US-10-142-421-258	Sequence 258, App
c 565	7	1.0	264	12	US-10-238-075-575	Sequence 575, App	c 638	7	1.0	406	12	US-10-142-432-66	Sequence 66, Appl
c 566	7	1.0	276	10	US-09-935-866-9	Sequence 9, Appli	c 639	7	1.0	406	12	US-10-142-432-258	Sequence 258, App
c 567	7	1.0	276	10	US-09-896-631A-15	Sequence 15, Appl	c 640	7	1.0	406	12	US-10-142-767-66	Sequence 66, Appl
c 568	7	1.0	280	10	US-09-960-631A-5	Sequence 5, Appli	c 641	7	1.0	406	12	US-10-142-767-258	Sequence 258, App
c 569	7	1.0	287	12	US-10-263-568-9	Sequence 9, Appli	c 642	7	1.0	406	12	US-10-143-033-66	Sequence 66, Appl
c 570	7	1.0	287	12	US-09-882-227-216	Sequence 216, App	c 643	7	1.0	406	12	US-10-143-033-258	Sequence 258, App
c 571	7	1.0	294	12	US-10-017-161-2318	Sequence 2318, App	c 644	7	1.0	406	12	US-10-144-994-66	Sequence 66, Appl
c 572	7	1.0	298	12	US-10-017-161-2194	Sequence 2194, App	c 645	7	1.0	406	12	US-10-144-994-258	Sequence 258, App
c 573	7	1.0	315	12	US-10-017-161-1060	Sequence 1060, App	c 646	7	1.0	406	12	US-10-145-628-66	Sequence 66, Appl
c 574	7	1.0	316	15	US-10-156-761-11477	Sequence 11477, A	c 647	7	1.0	406	12	US-10-145-628-258	Sequence 258, App
c 575	7	1.0	319	12	US-10-032-201B-278	Sequence 278, App	c 648	7	1.0	406	12	US-10-145-631-66	Sequence 66, Appl
c 576	7	1.0	326	12	US-10-032-201B-280	Sequence 280, App	c 649	7	1.0	406	12	US-10-145-631-258	Sequence 258, App
c 577	7	1.0	326	12	US-10-289-757-112	Sequence 112, App	c 650	7	1.0	406	12	US-10-145-633-66	Sequence 66, Appl
c 578	7	1.0	328	15	US-10-156-761-9579	Sequence 9579, App	c 651	7	1.0	406	12	US-10-145-633-258	Sequence 258, App
c 579	7	1.0	333	11	US-09-769-787-43	Sequence 43, Appl	c 652	7	1.0	406	12	US-10-145-746-66	Sequence 66, Appl
c 580	7	1.0	333	12	US-10-017-161-2102	Sequence 2102, App	c 653	7	1.0	406	12	US-10-145-746-258	Sequence 258, App
c 581	7	1.0	337	10	US-09-866-230-8	Sequence 8, Appli	c 654	7	1.0	406	12	US-10-145-748-66	Sequence 66, Appl
c 582	7	1.0	337	10	US-09-868-478-5	Sequence 5, Appli	c 655	7	1.0	406	12	US-10-145-748-258	Sequence 258, App
c 583	7	1.0	337	12	US-09-991-225-6	Sequence 6, Appli	c 656	7	1.0	406	12	US-10-145-823-66	Sequence 66, Appl
c 584	7	1.0	337	12	US-10-349-021-5	Sequence 5, Appli	c 657	7	1.0	406	12	US-10-145-823-258	Sequence 258, App

658	7	1.0	406	12	US-10-145-826-66	Sequence 66, Appl	731	7	1.0	406	12	US-10-142-424-66	Sequence 66, Appl
659	7	1.0	406	12	US-10-145-826-258	Sequence 258, App	732	7	1.0	406	12	US-10-142-424-258	Sequence 258, App
660	7	1.0	406	12	US-10-145-870-66	Sequence 66, Appl	733	7	1.0	406	12	US-10-143-761-66	Sequence 66, Appl
661	7	1.0	406	12	US-10-145-870-258	Sequence 258, App	734	7	1.0	406	12	US-10-142-761-258	Sequence 258, App
662	7	1.0	406	12	US-10-145-876-66	Sequence 66, Appl	735	7	1.0	406	12	US-10-142-763-66	Sequence 66, Appl
663	7	1.0	406	12	US-10-145-876-258	Sequence 258, App	736	7	1.0	406	12	US-10-142-763-258	Sequence 258, App
664	7	1.0	406	12	US-10-145-959-66	Sequence 66, Appl	737	7	1.0	406	12	US-10-142-765-66	Sequence 66, Appl
665	7	1.0	406	12	US-10-145-959-258	Sequence 258, App	738	7	1.0	406	12	US-10-142-765-258	Sequence 258, App
666	7	1.0	406	12	US-10-146-724-66	Sequence 66, Appl	739	7	1.0	406	12	US-10-142-887-66	Sequence 66, Appl
667	7	1.0	406	12	US-10-146-724-258	Sequence 258, App	740	7	1.0	406	12	US-10-143-887-258	Sequence 258, App
668	7	1.0	406	12	US-10-146-725-66	Sequence 66, Appl	741	7	1.0	406	12	US-10-143-888-66	Sequence 66, Appl
669	7	1.0	406	12	US-10-146-725-258	Sequence 258, App	742	7	1.0	406	12	US-10-142-888-258	Sequence 258, App
670	7	1.0	406	12	US-10-146-735-66	Sequence 66, Appl	743	7	1.0	406	12	US-10-143-034-66	Sequence 66, Appl
671	7	1.0	406	12	US-10-146-735-258	Sequence 258, App	744	7	1.0	406	12	US-10-143-034-258	Sequence 258, App
672	7	1.0	406	12	US-10-147-495-66	Sequence 66, Appl	745	7	1.0	406	12	US-10-143-116-66	Sequence 66, Appl
673	7	1.0	406	12	US-10-147-495-258	Sequence 258, App	746	7	1.0	406	12	US-10-143-116-258	Sequence 258, App
674	7	1.0	406	12	US-10-147-501-66	Sequence 66, Appl	747	7	1.0	406	12	US-10-144-957-66	Sequence 66, Appl
675	7	1.0	406	12	US-10-147-501-258	Sequence 258, App	748	7	1.0	406	12	US-10-144-957-258	Sequence 258, App
676	7	1.0	406	12	US-10-147-504-66	Sequence 66, Appl	749	7	1.0	406	12	US-10-144-992-66	Sequence 66, Appl
677	7	1.0	406	12	US-10-147-504-258	Sequence 258, App	750	7	1.0	406	12	US-10-144-992-258	Sequence 258, App
678	7	1.0	406	12	US-10-147-506-66	Sequence 66, Appl	751	7	1.0	406	12	US-10-145-015-66	Sequence 66, Appl
679	7	1.0	406	12	US-10-147-506-258	Sequence 258, App	752	7	1.0	406	12	US-10-145-015-258	Sequence 258, App
680	7	1.0	406	12	US-10-147-509-66	Sequence 66, Appl	753	7	1.0	406	12	US-10-145-090-66	Sequence 66, Appl
681	7	1.0	406	12	US-10-147-509-258	Sequence 258, App	754	7	1.0	406	12	US-10-145-090-258	Sequence 258, App
682	7	1.0	406	12	US-10-147-510-66	Sequence 66, Appl	755	7	1.0	406	12	US-10-145-091-66	Sequence 66, Appl
683	7	1.0	406	12	US-10-147-510-258	Sequence 258, App	756	7	1.0	406	12	US-10-145-091-258	Sequence 258, App
684	7	1.0	406	12	US-10-147-511-66	Sequence 66, Appl	757	7	1.0	406	12	US-10-145-623-66	Sequence 66, Appl
685	7	1.0	406	12	US-10-147-511-258	Sequence 258, App	758	7	1.0	406	12	US-10-145-623-258	Sequence 258, App
686	7	1.0	406	12	US-10-147-529-66	Sequence 66, Appl	759	7	1.0	406	12	US-10-145-630-66	Sequence 66, Appl
687	7	1.0	406	12	US-10-147-529-258	Sequence 258, App	760	7	1.0	406	12	US-10-145-630-258	Sequence 258, App
688	7	1.0	406	12	US-10-152-397-66	Sequence 66, Appl	761	7	1.0	406	12	US-10-145-747-66	Sequence 66, Appl
689	7	1.0	406	12	US-10-152-397-258	Sequence 258, App	762	7	1.0	406	12	US-10-145-747-258	Sequence 258, App
690	7	1.0	406	12	US-10-153-586-66	Sequence 66, Appl	763	7	1.0	406	12	US-10-145-752-66	Sequence 66, Appl
691	7	1.0	406	12	US-10-153-586-258	Sequence 258, App	764	7	1.0	406	12	US-10-145-752-258	Sequence 258, App
692	7	1.0	406	12	US-10-158-783-66	Sequence 66, Appl	765	7	1.0	406	12	US-10-145-752-66	Sequence 66, Appl
693	7	1.0	406	12	US-10-158-783-258	Sequence 258, App	766	7	1.0	406	12	US-10-145-754-66	Sequence 258, App
694	7	1.0	406	12	US-10-158-786-66	Sequence 66, Appl	767	7	1.0	406	12	US-10-145-753-66	Sequence 66, Appl
695	7	1.0	406	12	US-10-158-786-258	Sequence 258, App	768	7	1.0	406	12	US-10-145-755-258	Sequence 258, App
696	7	1.0	406	12	US-10-140-019-66	Sequence 66, Appl	769	7	1.0	406	12	US-10-145-818-66	Sequence 66, Appl
697	7	1.0	406	12	US-10-140-019-258	Sequence 258, App	770	7	1.0	406	12	US-10-145-818-258	Sequence 258, App
698	7	1.0	406	12	US-10-140-022-66	Sequence 66, Appl	771	7	1.0	406	12	US-10-145-820-66	Sequence 66, Appl
699	7	1.0	406	12	US-10-140-022-258	Sequence 258, App	772	7	1.0	406	12	US-10-145-820-258	Sequence 258, App
700	7	1.0	406	12	US-10-140-861-66	Sequence 66, Appl	773	7	1.0	406	12	US-10-145-872-66	Sequence 66, Appl
701	7	1.0	406	12	US-10-140-861-258	Sequence 258, App	774	7	1.0	406	12	US-10-145-872-258	Sequence 258, App
702	7	1.0	406	12	US-10-140-862-66	Sequence 66, Appl	775	7	1.0	406	12	US-10-145-873-66	Sequence 66, Appl
703	7	1.0	406	12	US-10-140-862-258	Sequence 258, App	776	7	1.0	406	12	US-10-145-873-258	Sequence 258, App
704	7	1.0	406	12	US-10-141-697-66	Sequence 66, Appl	777	7	1.0	406	12	US-10-147-481-66	Sequence 66, Appl
705	7	1.0	406	12	US-10-141-697-258	Sequence 258, App	778	7	1.0	406	12	US-10-147-481-258	Sequence 258, App
706	7	1.0	406	12	US-10-141-700-66	Sequence 66, Appl	779	7	1.0	406	12	US-10-147-482-66	Sequence 66, Appl
707	7	1.0	406	12	US-10-141-700-258	Sequence 258, App	780	7	1.0	406	12	US-10-147-482-258	Sequence 258, App
708	7	1.0	406	12	US-10-141-705-66	Sequence 66, Appl	781	7	1.0	406	12	US-10-147-503-66	Sequence 66, Appl
709	7	1.0	406	12	US-10-141-705-258	Sequence 258, App	782	7	1.0	406	12	US-10-147-503-258	Sequence 258, App
710	7	1.0	406	12	US-10-141-753-66	Sequence 66, Appl	783	7	1.0	406	12	US-10-147-522-66	Sequence 66, Appl
711	7	1.0	406	12	US-10-141-753-258	Sequence 258, App	784	7	1.0	406	12	US-10-147-522-258	Sequence 258, App
712	7	1.0	406	12	US-10-141-758-66	Sequence 66, Appl	785	7	1.0	406	12	US-10-152-401-66	Sequence 66, Appl
713	7	1.0	406	12	US-10-141-758-258	Sequence 258, App	786	7	1.0	406	12	US-10-152-401-258	Sequence 258, App
714	7	1.0	406	12	US-10-142-438-66	Sequence 66, Appl	787	7	1.0	406	12	US-10-157-783-66	Sequence 66, Appl
715	7	1.0	406	12	US-10-142-438-258	Sequence 258, App	788	7	1.0	406	12	US-10-157-783-258	Sequence 258, App
716	7	1.0	406	12	US-10-142-440-66	Sequence 66, Appl	789	7	1.0	406	12	US-10-157-783-66	Sequence 66, Appl
717	7	1.0	406	12	US-10-142-440-258	Sequence 258, App	790	7	1.0	406	12	US-10-158-463-66	Sequence 258, App
718	7	1.0	406	12	US-10-143-422-66	Sequence 66, Appl	791	7	1.0	406	12	US-10-158-463-258	Sequence 258, App
719	7	1.0	406	12	US-10-143-422-258	Sequence 258, App	792	7	1.0	406	12	US-10-158-793-66	Sequence 258, App
720	7	1.0	406	12	US-10-143-427-66	Sequence 66, Appl	793	7	1.0	406	12	US-10-158-793-258	Sequence 258, App
721	7	1.0	406	12	US-10-143-427-258	Sequence 258, App	794	7	1.0	406	12	US-10-143-035-66	Sequence 258, App
722	7	1.0	406	12	US-10-143-437-66	Sequence 66, Appl	795	7	1.0	406	12	US-10-143-035-258	Sequence 258, App
723	7	1.0	406	12	US-10-143-437-258	Sequence 258, App	796	7	1.0	406	12	US-10-143-035-66	Sequence 66, Appl
724	7	1.0	406	12	US-10-143-760-66	Sequence 66, Appl	797	7	1.0	406	12	US-10-143-751-66	Sequence 66, Appl
725	7	1.0	406	12	US-10-143-760-258	Sequence 258, App	798	7	1.0	406	12	US-10-143-751-258	Sequence 258, App
726	7	1.0	406	12	US-10-145-821-66	Sequence 66, Appl	799	7	1.0	406	12	US-10-145-822-66	Sequence 66, Appl
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730	7	1.0	406	12	US-09-876-997-66	Sequence 258, App	803	7	1.0	406	12	US-10-145-821-66	Sequence 66, Appl
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734	7	1.0	406	12	US-10-127-840A-66	Sequence 66, Appl	807	7	1.0	406	12	US-10-145-869-66	Sequence 66, Appl
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806	7	1.0	406	12	US-10-145-875-258	Sequence 258, App	879	7	1.0	406	12	US-10-157-784-258	Sequence 258, App
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857	7	1.0	406	12	US-10-147-491-66	Sequence 66, App	930	7	1.0	406	12	US-10-123-906-66	Sequence 258, App
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## ALIGNMENTS

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US-10-163-866-48
; Sequence 48, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
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; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-48

Alignment Scores:
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Score: 466.00 Matches: 466
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.66% Indels: 0
DB: 15 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-163-866-48 (1-501)

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## RESULT 2

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US-10-163-866-49
; Sequence 49, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SUC7B AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 501
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-163-866-49
Alignment Scores:
Pred. No.: 0 Length: 501
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Score: 466.00 Matches: 466
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 63.66% Indels: 0
DB: 15 Gaps: 0
US-09-667-170A-440 (1-2239) x US-10-163-866-49 (1-501)
QY 334 GAGAAAGTCGAGCTCAGAGAGAAAGTCATTTACTAGGGGAGTCTCCATTATCATGGC 393
Db 36 GluLysValGlnLeuLysArgLysValThrLeuLeuArgGlyValSerIleIleIleGly 55
QY 394 ACCATCATTTGAGCAGGAATCTTCATCTCTCTAAGGGCGTCCAGAACACGGGAGC 453
Db 56 ThrIleIleGlyAlaGlyIlePheIleSerProLysGlyValLeuGlnAsnThrGlySer 75
QY 454 GTGGGCGATGCTCTGACATCTGGACGGTGTGTGGGTCTCTGTCACATATTTGGAGCTTTG 513
Db 76 ValGlyMetSerLeuThrIleTrpThrValCysGlyValLeuSerLeuPheGlyAlaLeu 95
QY 514 TCTTATGCTGAATTCGGAACAACTATAAGAAATCTCGAGGTCAATTACATATATTTTG 573
Db 96 SerTyrAlaGluLeuGlyThrThrIleLysLysSerGlyGlyHisTyrThrTyrIleLeu 115
QY 574 GAAGTCTTTGGTCCATTACCAAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATATACGC 633
Db 116 GluValPheGlyProLeuProAlaPheValArgValTrpValGluLeuLeuIleIleArg 135
QY 634 CTGCGACGTACTGCTGTGATATCCCTGGCATTTGGACGTACATTTCTGGAACCATTTT 693
Db 136 ProAlaIleThrAlaValIleSerLeuAlaPheGlyArgTyrIleLeuGluProPhePhe 155
QY 694 ATTCAATGTCAATCCCTGCACTTCGATCAAGCTCAATACAGCTGGCGCATTAACCTGTA 753
Db 156 IleGlnCysGluIleProGluLeuAlaIleLysLeuIleThrAlaValGlyIleThrVal 175
QY 754 GTGATGTCTCTAAATAGCATGAGTGTGAGTGGAGCGCCCGGATCCAGATTTTCTTAACC 813
Db 176 ValMetValLeuAsnSerMetSerValSerTrpSerAlaArgIleGlnIlePheLeuThr 195
QY 814 TTTTGAAGCTCAGCAATCTGATTAATATATAGTCCCTGGAGTTATGCGAGCTAATTA 873
Db 196 PheCysLysLeuThrAlaIleLeuIleIleValProGlyValMetGlnLeuIleLys 215
QY 874 GGTCAAAACGACAGACTTTAAGACGCTTTTCGGAAGAGATTCAGATTAATACGGGTG 933
Db 216 GlyGlnThrGlnAsnPheLysAspAlaPheSerGlyArgAspSerIleThrArgLeu 235
QY 934 CCACTGGCTTTTATTATGGAATGTATGATATGCTATGCTGGCTGGTTTACCTCAACTTTGTT 993
Db 236 ProLeuAlaPheTyrTyrGlyMetTyrAlaTyrAlaGlyTrpPheTyrLeuAsnPheVal 255
QY 994 ACTGAAGAAGTAGAAAACCCCTGAAAACCATTTCCCTTCCATATATATATCATCGGCC 1053
Db 256 ThrGluGluValGluAsnProGluLysThrIleProLeuAlaIleCysIleSerMetAla 275
QY 1054 ATTGTACCACTTGGCTATGCTGACAAATGTGCGCTACTTTTACGACATTAATGCTGAG 1113
Db 276 IleValThrIleGlyTyrValLeuThrAsnValAlaTyrPheThrThrIleAsnAlaGlu 295
QY 1114 GAGCTGCTGCTTTCAAATGCAGTGGCAGTGCACCTTTTCTGAGCGGCTACTGGGAAATTC 1173
Db 296 GluLeuLeuLeuSerAsnAlaValAlaValThrPheSerGluArgLeuLeuGlyAsnPhe 315
QY 1174 TCATTAGAGTTCGATCTTGTGCTCTCTCTCTCTGCTCCATGACGGTGGTG 1233
Db 316 SerLeuAlaValProIlePheValAlaLeuSerCysPheGlySerMetAsnGlyVal 335
QY 1234 TTTGCTGCTCCAGGTATTCTATGTTGGTCTCGAGAGGGTCACTTCCAGAAATCCTC 1293
Db 336 PheAlaValSerArgLeuPheTyrValAlaSerArgGluGlyHisLeuProGluIleLeu 355
QY 1294 TCCATGATTCATGTCGCAAGCACACTCTCTCTACCAGTCTTATTGTTTGGACCCCTTTG 1353
```



; Sequence 586, Application US/10144649A  
; Publication No. US20030118599A1  
; GENERAL INFORMATION:  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Pan, Liqun  
; APPLICANT: Algate, Paul A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.475C11  
; CURRENT APPLICATION NUMBER: US/10/144,649A  
; NUMBER OF SEQ ID NOS: 749  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 586  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-144-649A-586

Alignment Scores:  
Pred. No.: 5,93e-83 Length: 97  
Score: 93.00 Matches: 93  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.70% Indels: 0  
DB: 15 Gaps: 0  
US-09-667-170A-440 (1-2239) x US-10-144-649A-586 (1-97)

QY 2 GAGTTGAAGTGAGCAGAGATCATCCAGCTGGTGACAGTGAGACTCTGTCTCAAAACA 61  
Db 1 GluValGluValSerArgAspHisAlaSerLeuGlyAspSerGluThrLeuSerGlnThr 20  
QY 62 GAATTAAGGAAAAAAGAAAGAAAGAAAGAGAGAGAGAAATTCAGGCCAATTGTGGC 121  
Db 21 GluLeuArgLysLysGluArgLysLysLysArgGluArgLysPheGlnAlaAsnCysGly 40  
QY 122 ATAGATTTTATCATATTTCTGGATTTTGGATTCTTTGTTTCTCATCTGAGTTTCTG 181  
Db 41 IleaspPheIlellePheTrpIlePheTrpIleLeuLeuPheSerHisTrpIleGln 60  
QY 182 GAAAGCCTGTGTGTCCACCATCTCCAAAGGAGGTACCTGAGGAGAAATGTTAAACGGGA 241  
Db 61 GluSerLeuLeuCysProSerProLysGluValThrCysArgGluMetLeuThrGly 80  
QY 242 GGCTGCCTTCCTGGGCAACAGGAGCCACCTGGGCAGG 280  
Db 81 GlyCysLeuProTrpAlaThrArgSerHisLeuGlyArg 93

RESULT 6  
US-10-144-649A-742  
; Sequence 742, Application US/10144649A  
; Publication No. US20030118599A1  
; GENERAL INFORMATION:  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Pan, Liqun  
; APPLICANT: Algate, Paul A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.475C11  
; CURRENT APPLICATION NUMBER: US/10/144,649A  
; CURRENT FILING DATE: 2002-08-21  
; NUMBER OF SEQ ID NOS: 749  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 742  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-144-649A-742

Alignment Scores:  
Pred. No.: 5,84e-83 Length: 114  
Score: 93.00 Matches: 93  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.70% Indels: 0  
DB: 15 Gaps: 0  
US-09-667-170A-440 (1-2239) x US-10-144-649A-742 (1-114)  
QY 2 GAGTTGAAGTGAGCAGAGATCATCCAGCTGGTGACAGTGAGACTCTGTCTCAAAACA 61  
Db 18 GluValGluValSerArgAspHisAlaSerLeuGlyAspSerGluThrLeuSerGlnThr 37  
QY 62 GAATTAAGGAAAAAAGAAAGAAAGAAAGAGAGAGAGAAATTCAGGCCAATTGTGGC 121  
Db 38 GluLeuArgLysLysGluArgLysLysLysArgGluArgLysPheGlnAlaAsnCysGly 57  
QY 122 ATAGATTTTATCATATTTCTGGATTTTGGATTCTTTGTTTCTCATCTGAGTTTCTG 181  
Db 58 IleaspPheIlellePheTrpIlePheTrpIleLeuLeuPheSerHisTrpIleGln 77  
QY 182 GAAAGCCTGTGTGTCCACCATCTCCAAAGGAGGTACCTGAGGAGAAATGTTAAACGGGA 241  
Db 78 GluSerLeuLeuCysProSerProLysGluValThrCysArgGluMetLeuThrGly 97  
QY 242 GGCTGCCTTCCTGGGCAACAGGAGCCACCTGGGCAGG 280  
Db 98 GlyCysLeuProTrpAlaThrArgSerHisLeuGlyArg 110

RESULT 7  
US-10-214-867A-13  
; Sequence 13, Application US/10214867A  
; Publication No. US2003014844A1  
; GENERAL INFORMATION:  
; APPLICANT: ENDOU, HITOSHI  
; APPLICANT: KANAI, YOSHIKATSU  
; TITLE OF INVENTION: SODIUM-INDEPENDENT SMALL NEUTRAL AMINO ACID  
; TRANSPORTERS TRANSPORTING L- AND D-AMINO ACIDS AND  
; FILE REFERENCE: 57783 (71526)  
; CURRENT APPLICATION NUMBER: US/10/214,867A  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: JP 2000-28822  
; PRIOR FILING DATE: 2000-02-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Murine sp.  
US-10-214-867A-13  
Alignment Scores:  
Pred. No.: 2,36e-36 Length: 502  
Score: 46.00 Matches: 46  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 6.28% Indels: 0  
DB: 12 Gaps: 0  
US-09-667-170A-440 (1-2239) x US-10-214-867A-13 (1-502)

QY 1171 TTCTCATTAGCAGTCCGATCTTTGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230  
Db 315 PheSerLeuAlaValProIlePheValAlaLeuSerCysPheGlySerMetAsnGlyGly 334  
QY 1231 GTGTTGCTCTCTCCAGGTTATTTCTATGTTGCGTCTCGAGAGGTTACCTTCCAGAAATC 1290  
Db 335 ValPheAlaValSerArgLeuPheTyrValAlaSerArgGluGlyHisLeuProGluIle 354

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QY 1291 CTCCTCATGATTCATGTC 1308
Db 355 LeuSerMetIleHisVal 360

RESULT 8
US-09-738-973-587
; Sequence 587, Application US/09738973
; Patent No. US20020110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Elliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 587
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-738-973-587

Alignment Scores:
Pred. No.: 1.96e-06 Length: 16
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.19% Indels: 0
DB: 10 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-738-973-587 (1-16)
QY 104 TTCAGGCCAATTGGCATAGATTTATCATATTCGATTTTGG 151
Db 1 PheGlnAlaAsnCysGlyIleAspPheIleIlePheTrpIlePheTrp 16

RESULT 9
US-09-854-133-587
; Sequence 587, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 587
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-133-587

Alignment Scores:
Pred. No.: 1.96e-06 Length: 16
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.19% Indels: 0
DB: 10 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-738-973-587 (1-16)
QY 104 TTCAGGCCAATTGGCATAGATTTATCATATTCGATTTTGG 151
Db 1 PheGlnAlaAsnCysGlyIleAspPheIleIlePheTrpIlePheTrp 16

RESULT 10
US-10-144-649A-587
; Sequence 587, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 587
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-649A-587

Alignment Scores:
Pred. No.: 1.96e-06 Length: 16
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.19% Indels: 0
DB: 15 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-144-649A-587 (1-16)
QY 104 TTCAGGCCAATTGGCATAGATTTATCATATTCGATTTTGG 151
Db 1 PheGlnAlaAsnCysGlyIleAspPheIleIlePheTrpIlePheTrp 16

RESULT 11
US-10-029-386-32531
; Sequence 32531, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32531
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL135998.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
```

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3  
; OTHER INFORMATION: SWISSPROT HIT: Q9UM01, EVALUE 9.00e-83  
US-10-029-386-32531

Alignment Scores:  
Pred. No.: 0.0149 Length: 166  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.64% Indels: 0  
DB: 12 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-029-386-32531 (1-166)

Qy 517 TATGCTGAATTGGGAACAACATAAAGAAATCTGGA 552  
|||||  
Db 90 TyrAlaGluLeuGlyThrThrIleLysSerGly 101

## RESULT 12

US-10-214-867A-11  
; Sequence 11, Application US/10214867A  
; Publication No. US2003014844A1  
; GENERAL INFORMATION:  
; APPLICANT: ENDOW, HITOSHI  
; TITLE OF INVENTION: SODIUM-INDEPENDENT SMALL NEUTRAL AMINO ACID  
; TITLE OF INVENTION: TRANSPORTERS TRANSPORTING L- AND D-AMINO ACIDS AND  
; TITLE OF INVENTION: GENES THEREOF  
; FILE REFERENCE: 57783 (71526)  
; CURRENT APPLICATION NUMBER: US/10/214, 867A  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: PCT/JP01/00031  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: JP 2000-28822  
; PRIOR FILING DATE: 2000-02-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 511  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-214-867A-11

Alignment Scores:  
Pred. No.: 0.0134 Length: 511  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.64% Indels: 0  
DB: 12 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-214-867A-11 (1-511)

Qy 517 TATGCTGAATTGGGAACAACATAAAGAAATCTGGA 552  
|||||  
Db 90 TyrAlaGluLeuGlyThrThrIleLysSerGly 101

## RESULT 13

US-10-163-866-41  
; Sequence 41, Application US/10163866  
; Publication No. US20030027188A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: SLCTs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-080C  
; CURRENT APPLICATION NUMBER: US/10/163,866  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605

; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/338,733  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/357,600  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 41  
; LENGTH: 511  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-163-866-41

Alignment Scores:  
Pred. No.: 0.0134 Length: 511  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.64% Indels: 0  
DB: 15 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-163-866-41 (1-511)

Qy 517 TATGCTGAATTGGGAACAACATAAAGAAATCTGGA 552  
|||||  
Db 90 TyrAlaGluLeuGlyThrThrIleLysSerGly 101

## RESULT 14

US-10-163-866-42  
; Sequence 42, Application US/10163866  
; Publication No. US20030027188A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: SLCTs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-080C  
; CURRENT APPLICATION NUMBER: US/10/163,866  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/338,733  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/357,600  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 42  
; LENGTH: 511  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-163-866-42

Alignment Scores:  
Pred. No.: 0.0134 Length: 511  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.64% Indels: 0  
DB: 15 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-163-866-42 (1-511)

Qy 517 TATGCTGAATTGGGAACAACATAAAGAAATCTGGA 552  
|||||  
Db 90 TyrAlaGluLeuGlyThrThrIleLysSerGly 101

## RESULT 15

US-09-815-923-16

```
; Sequence 16, Application US/09815923
; Publication No. US20020197644A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Sarjeet S.
; APPLICANT: Ross, Linda S.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A1
; TITLE OF INVENTION: Target Sites for Insecticides
; FILE REFERENCE: 023070-093800US
; CURRENT APPLICATION NUMBER: US/09/815,923
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Aedes aegypti
; FEATURE:
; OTHER INFORMATION: LAT transporter
US-09-815-923-16
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Alignment Scores:
Pred. No.: 0.132 Length: 517
Score: 31.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.50% Indels: 0
DB: 10 Gaps: 0
```

US-09-667-170A-440 (1-2239) x US-09-815-923-16 (1-517)

```
QY 409 GGAATCTTCATCTCTCTAAGCGCTGCTCCAG 441
Db ||||| ||||| ||||| ||||| ||||| |||||
74 GlyIlePheIleSerProLysGlyValLeuGln 84
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Search completed: October 31, 2003, 12:25:22  
Job time : 172 secs